

Sequence Listing

- <110> Ashkenazi, Avi J.
 Baker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Gerber, Hanspeter
 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Kljavin, Ivar J.
 Napier, Mary A.
 Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Stewart, Timothy A.
 Tumas, Daniel
 Watanabe, Colin K.
 Williams, P. Mickey
 Wood, William I.
 Zhang, Zemin
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 <213> Homo sapiens

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 35 40 45
 Val Ile Thr Pro Gly Ser Pro Glu Pro Val Ile Leu Val Ala Cys
 50 55 60
 Val Pro Leu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu Thr Tyr
 65 70 75
 Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu
 80 85 90
 Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln
 95 100 105
 Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala
 110 115 120
 Ile Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys
 125 130 135
 Ala Met Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile
 140 145 150

Arg	Ile	Ile	Gln	Glu	Arg	Asn	Gly	Val	Leu	Pro	Asp	Cys	Leu	Thr
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Asp	Gly	Ser	Asp	Val	Val	Ser	Asp	Leu	Glu	His	Glu	Glu	Met	Lys
				170					175					180
Ile	Leu	Arg	Glu	Val	Leu	Arg	Lys	Ser	Lys	Glu	Glu	Tyr	Asp	Gln
				185					190					195
Glu	Glu	Glu	Arg	Lys	Arg	Lys	Lys	Gln	Leu	Ser	Glu	Ala	Lys	Thr
				200					205					210
Glu	Glu	Pro	Thr	Val	His	Ser	Ser	Glu	Ala	Ala	Ile	Met	Asn	Asn
				215					220					225
Ser	Gln	Gly	Asp	Gly	Glu	His	Phe	Ala	His	Pro	Pro	Ser	Glu	Val
				230					235					240
Lys	Met	His	Phe	Ala	Asn	Gln	Ser	Ile	Glu	Pro	Leu	Gly	Arg	Lys
				245					250					255
Val	Glu	Arg	Ser	Glu	Thr	Ser	Ser	Leu	Pro	Gln	Lys	Gly	Leu	Lys
				260					265					270
Ile	Pro	Gly	Leu	Glu	His	Ala	Ser	Ile	Glu	Gly	Pro	Ile	Ala	Asn
				275					280					285
Leu	Ser	Val	Leu	Gly	Thr	Glu	Glu	Leu	Arg	Gln	Arg	Glu	His	Tyr
				290					295					300
Leu	Lys	Gln	Lys	Arg	Asp	Lys	Leu	Met	Ser	Met	Arg	Lys	Asp	Met
				305					310					315
Arg	Thr	Lys	Gln	Ile	Gln	Asn	Met	Glu	Gln	Lys	Gly	Lys	Pro	Thr
				320					325					330
Gly	Glu	Val	Glu	Glu	Met	Thr	Glu	Lys	Pro	Glu	Met	Thr	Ala	Glu
				335					340					345
Glu	Lys	Gln	Thr	Leu	Leu	Lys	Arg	Arg	Leu	Leu	Ala	Glu	Lys	Leu
				350					355					360
Lys	Glu	Glu	Val	Ile	Asn	Lys								
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 <211> 418
 <212> DNA
 <213> Homo sapiens

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 tgcacttctc ctcttgcaaa gacccatata tcacaggcca tttttgcaac 200
 ctgtgttggc agcagaagat ttactatct ttaaagcaat gatggtccag 250
 aaaaacattg aaatgcagct gcaagccatt cgaataattc aagagagaaa 300

tggtgtatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350
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gaggaatatg accaggaa 418

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 10
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<210> 11
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<212> DNA
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<220>
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<400> 11
ctaagaactt ccctcaggat ttt 23

<210> 12
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
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<210> 13
<211> 2886
<212> DNA
<213> Homo sapiens

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cactagaagc tcttctgagg gaggttaatta aaaaacagtg gaatggaaaa 200
acagtgcctgt agtcatcctg taatatgctc cttgtcaaca atgtatacat 250
tctgctagg tgccatattc attgctttaa gctcaagtcg catcttacta 300
gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 350
tgtgaatgtg tgctcagaac tggatgaagct agttttctgt gtgcttgtgt 400
cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 450

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 ttatttctctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 550
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 cttattttca cattttcagt gtttgaata tttatctttt cactttgata 1550
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<210> 14

<211> 424

<212> PRT

<213> Homo sapiens

<400> 14

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Thr	Met	Tyr	Thr	Phe	Leu	Leu	Gly	Ala	Ile	Phe	Ile	Ala	Leu	Ser
				20					25					30
Ser	Ser	Arg	Ile	Leu	Leu	Val	Lys	Tyr	Ser	Ala	Asn	Glu	Glu	Asn
				35					40					45
Lys	Tyr	Asp	Tyr	Leu	Pro	Thr	Thr	Val	Asn	Val	Cys	Ser	Glu	Leu
				50					55					60
Val	Lys	Leu	Val	Phe	Cys	Val	Leu	Val	Ser	Phe	Cys	Val	Ile	Lys
				65					70					75
Lys	Asp	His	Gln	Ser	Arg	Asn	Leu	Lys	Tyr	Ala	Ser	Trp	Lys	Glu
				80					85					90
Phe	Ser	Asp	Phe	Met	Lys	Trp	Ser	Ile	Pro	Ala	Phe	Leu	Tyr	Phe
				95					100					105
Leu	Asp	Asn	Leu	Ile	Val	Phe	Tyr	Val	Leu	Ser	Tyr	Leu	Gln	Pro
				110					115					120

Ala Met Ala Val	Ile Phe Ser Asn Phe	Ser Ile Ile Thr Thr	Ala
	125	130	135
Leu Leu Phe Arg	Ile Val Leu Lys Arg	Arg Leu Asn Trp Ile	Gln
	140	145	150
Trp Ala Ser Leu	Leu Thr Leu Phe Leu	Ser Ile Val Ala Leu	Thr
	155	160	165
Ala Gly Thr Lys	Thr Leu Gln His Asn	Leu Ala Gly Arg Gly	Phe
	170	175	180
His His Asp Ala	Phe Phe Ser Pro Ser	Asn Ser Cys Leu Leu	Phe
	185	190	195
Arg Ser Glu Cys	Pro Arg Lys Asp Asn	Cys Thr Ala Lys Glu	Trp
	200	205	210
Thr Phe Pro Glu	Ala Lys Trp Asn Thr	Thr Ala Arg Val Phe	Ser
	215	220	225
His Ile Arg Leu	Gly Met Gly His Val	Leu Ile Ile Val Gln	Cys
	230	235	240
Phe Ile Ser Ser	Met Ala Asn Ile Tyr	Asn Glu Lys Ile Leu	Lys
	245	250	255
Glu Gly Asn Gln	Leu Thr Glu Ser Ile	Phe Ile Gln Asn Ser	Lys
	260	265	270
Leu Tyr Phe Phe	Gly Ile Leu Phe Asn	Gly Leu Thr Leu Gly	Leu
	275	280	285
Gln Arg Ser Asn	Arg Asp Gln Ile Lys	Asn Cys Gly Phe Phe	Tyr
	290	295	300
Gly His Ser Ala	Phe Ser Val Ala Leu	Ile Phe Val Thr Ala	Phe
	305	310	315
Gln Gly Leu Ser	Val Ala Phe Ile Leu	Lys Phe Leu Asp Asn	Met
	320	325	330
Phe His Val Leu	Met Ala Gln Val Thr	Thr Val Ile Ile Thr	Thr
	335	340	345
Val Ser Val Leu	Val Phe Asp Phe Arg	Pro Ser Leu Glu Phe	Phe
	350	355	360
Leu Glu Ala Pro	Ser Val Leu Leu Ser	Ile Phe Ile Tyr Asn	Ala
	365	370	375
Ser Lys Pro Gln	Val Pro Glu Tyr Ala	Pro Arg Gln Glu Arg	Ile
	380	385	390
Arg Asp Leu Ser	Gly Asn Leu Trp Glu	Arg Ser Ser Gly Asp	Gly
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Glu Glu Leu Glu	Arg Leu Thr Lys Pro	Lys Ser Asp Glu Ser	Asp
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Glu Asp Thr Phe			

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<211> 755
<212> DNA
<213> Homo sapiens

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ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 150
tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 200
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cagccatggc tggtatcttc tcaaatttta gcattataac aacagctctt 650
ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700
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cttta 755

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
ctatacctac tgtagcttct 20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcagagaatt ccttccagga 20

<210> 18
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgcctgt agtcatcctg taatatgctc cttgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

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<210> 20
 <211> 458
 <212> PRT
 <213> Homo sapiens

<400> 20
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 20 25 30
 Ala Ser Ala Asn Pro Pro Gly Pro Ala Trp Val Ala Leu Cys Pro
 35 40 45
 Gly Ser Ser Ser Pro Arg Pro Trp Pro Ser Leu Pro Thr Ser Ser
 50 55 60
 Ser Gly Ser Cys Pro Thr Ser His Thr Ala Arg Pro Ile Gly Thr
 65 70 75
 Cys Phe Ser Ile Ala Ser Leu Lys Gln Trp Ser Arg Val Ser Met
 80 85 90
 Phe Pro Thr Arg Leu Ser Pro Cys Ser Ser Ala Thr Glu Gln Thr
 95 100 105

Glu Arg Asp Ser	Ala 110	Thr Ala Tyr Arg	Met 115	Thr Val Glu Val	Leu 120
Gly Thr Val Leu	Gly 125	Thr Ala Ile Gln	Gly 130	Gln Ile Val Gly	Gln 135
Ala Asp Thr Pro	Cys 140	Phe Gln Asp Phe	Asn 145	Ser Ser Thr Val	Ala 150
Ser Gln Ser Ala	Asn 155	His Thr His Gly	Thr 160	Thr Ser His Arg	Glu 165
Thr Gln Lys Ala	Tyr 170	Leu Leu Ala Ala	Gly 175	Val Ile Val Cys	Ile 180
Tyr Ile Ile Cys	Ala 185	Val Ile Leu Ile	Leu 190	Gly Val Arg Glu	Gln 195
Arg Glu Pro Tyr	Glu 200	Ala Gln Gln Ser	Glu 205	Pro Ile Ala Tyr	Phe 210
Arg Gly Leu Arg	Leu 215	Val Met Ser His	Gly 220	Pro Tyr Ile Lys	Leu 225
Ile Thr Gly Phe	Leu 230	Phe Thr Ser Leu	Ala 235	Phe Met Leu Val	Glu 240
Gly Asn Phe Val	Leu 245	Phe Cys Thr Tyr	Thr 250	Leu Gly Phe Arg	Asn 255
Glu Phe Gln Asn	Leu 260	Leu Leu Ala Ile	Met 265	Leu Ser Ala Thr	Leu 270
Thr Ile Pro Ile	Trp 275	Gln Trp Phe Leu	Thr 280	Arg Phe Gly Lys	Lys 285
Thr Ala Val Tyr	Val 290	Gly Ile Ser Ser	Ala 295	Val Pro Phe Leu	Ile 300
Leu Val Ala Leu	Met 305	Glu Ser Asn Leu	Ile 310	Ile Thr Tyr Ala	Val 315
Ala Val Ala Ala	Gly 320	Ile Ser Val Ala	Ala 325	Ala Phe Leu Leu	Pro 330
Trp Ser Met Leu	Pro 335	Asp Val Ile Asp	Asp 340	Phe His Leu Lys	Gln 345
Pro His Phe His	Gly 350	Thr Glu Pro Ile	Phe 355	Phe Ser Phe Tyr	Val 360
Phe Phe Thr Lys	Phe 365	Ala Ser Gly Val	Ser 370	Leu Gly Ile Ser	Thr 375
Leu Ser Leu Asp	Phe 380	Ala Gly Tyr Gln	Thr 385	Arg Gly Cys Ser	Gln 390
Pro Glu Arg Val	Lys 395	Phe Thr Leu Asn	Met 400	Leu Val Thr Met	Ala 405
Pro Ile Val Leu	Ile 410	Leu Leu Gly Leu	Leu 415	Leu Phe Lys Met	Tyr 420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln
425 430 435

Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp
440 445 450

Ser Thr Glu Leu Ala Ser Ile Leu
455

<210> 21
<211> 571
<212> DNA
<213> Homo sapiens

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accctatgaa gccagcagt ctgagccaat cgcctacttc cggggcctac 150
ggctgggtcat gagccacggc ccatacatca aacttattac tggcttcctc 200
ttcacctcct tggctttcat gctggtggag gggaaactttg tttgtttttg 250
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tcatgctctc ggccacttta accattccca tctggcagtg gttcttgacc 350
cggtttgga agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400
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cggtagctgt ggagctggc atcagtgtgg cagctgcctt cttactaccc 500
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cttccatgga accgagccca t 571

<210> 22
<211> 1173
<212> DNA
<213> Homo sapiens

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aaacagaaaa cctgttagaa atgtggtggt ttcagcaagg cctcagtttc 150
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gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100
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<211> 266

<212> PRT

<213> Homo sapiens

<400> 23

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Val	Ile	Trp	Thr	Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala
				20					25					30
Val	Thr	Leu	His	His	Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp
				35					40					45
Thr	Gly	Thr	Val	Ala	Pro	Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu
				50					55					60
Asn	Ile	Ala	Ala	Val	Leu	Cys	Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr
				65					70					75
Lys	Gln	Val	His	Ala	Leu	Ser	Pro	Glu	Glu	Asn	Val	Ile	Ile	Lys
				80					85					90
Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Gly
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Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Lys	Thr	Thr	Leu	Phe	Ala	Ala
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His	Val	Ser	Gly	Ala	Val	Leu	Thr	Phe	Gly	Met	Gly	Ser	Leu	Tyr
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Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Ile
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His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val	Ile	Trp
						155								165
Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val	Leu
						170								180
His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp
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Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Val	Leu	His	Met	Ile	Thr	Thr	Ala
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Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr
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Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn
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Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 14, 484
 <223> unknown base

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 gagcggagat cctcaaacgg cctagtgttt cgcgcttccg gagaaaatca 150
 gcggtctaataaattcctct ggtttgttga agcagttacc aagaatcttc 200
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 gcaaggcctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400
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<211> 1399
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<213> Homo sapiens
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31

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 agcctggcca agatggtgaa atcctgtctc taataaaaaat acaaaaatta 1250
 gccaggcgtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300
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<211> 264

<212> PRT

<213> Homo sapiens

<400> 28

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Leu	Gly	Ser	Thr	Glu	Glu	Ala	Gly	Gly	Arg	Ser	Leu	Trp	Phe	Pro	35	40	45	
Ser	Asp	Leu	Ala	Glu	Leu	Arg	Glu	Leu	Ser	Glu	Val	Leu	Arg	Glu	50	55	60	
Tyr	Arg	Lys	Glu	His	Gln	Ala	Tyr	Val	Phe	Leu	Leu	Phe	Cys	Gly	65	70	75	
Ala	Tyr	Leu	Tyr	Lys	Gln	Gly	Phe	Ala	Ile	Pro	Gly	Ser	Ser	Phe	80	85	90	
Leu	Asn	Val	Leu	Ala	Gly	Ala	Leu	Phe	Gly	Pro	Trp	Leu	Gly	Leu	95	100	105	
Leu	Leu	Cys	Cys	Val	Leu	Thr	Ser	Val	Gly	Ala	Thr	Cys	Cys	Tyr	110	115	120	
Leu	Leu	Ser	Ser	Ile	Phe	Gly	Lys	Gln	Leu	Val	Val	Ser	Tyr	Phe	125	130	135	
Pro	Asp	Lys	Val	Ala	Leu	Leu	Gln	Arg	Lys	Val	Glu	Glu	Asn	Arg	140	145	150	
Asn	Ser	Leu	Phe	Phe	Phe	Leu	Leu	Phe	Leu	Arg	Leu	Phe	Pro	Met	155	160	165	
Thr	Pro	Asn	Trp	Phe	Leu	Asn	Leu	Ser	Ala	Pro	Ile	Leu	Asn	Ile	170	175	180	
Pro	Ile	Val	Gln	Phe	Phe	Phe	Ser	Val	Leu	Ile	Gly	Leu	Ile	Pro	185	190	195	
Tyr	Asn	Phe	Ile	Cys	Val	Gln	Thr	Gly	Ser	Ile	Leu	Ser	Thr	Leu	200	205	210	

Climatic data		Soil data		Plant data		Insect data	
Year	Month	Soil type	Soil depth (cm)	Plant species	Plant height (cm)	Insect species	Insect abundance
1998	Jan	1	10	1	10	1	10
1998	Feb	1	10	1	10	1	10
1998	Mar	1	10	1	10	1	10
1998	Apr	1	10	1	10	1	10
1998	May	1	10	1	10	1	10
1998	Jun	1	10	1	10	1	10
1998	Jul	1	10	1	10	1	10
1998	Aug	1	10	1	10	1	10
1998	Sep	1	10	1	10	1	10
1998	Oct	1	10	1	10	1	10
1998	Nov	1	10	1	10	1	10
1998	Dec	1	10	1	10	1	10
1999	Jan	1	10	1	10	1	10
1999	Feb	1	10	1	10	1	10
1999	Mar	1	10	1	10	1	10
1999	Apr	1	10	1	10	1	10
1999	May	1	10	1	10	1	10
1999	Jun	1	10	1	10	1	10
1999	Jul	1	10	1	10	1	10
1999	Aug	1	10	1	10	1	10
1999	Sep	1	10	1	10	1	10
1999	Oct	1	10	1	10	1	10
1999	Nov	1	10	1	10	1	10
1999	Dec	1	10	1	10	1	10
2000	Jan	1	10	1	10	1	10
2000	Feb	1	10	1	10	1	10
2000	Mar	1	10	1	10	1	10
2000	Apr	1	10	1	10	1	10
2000	May	1	10	1	10	1	10
2000	Jun	1	10	1	10	1	10
2000	Jul	1	10	1	10	1	10
2000	Aug	1	10	1	10	1	10
2000	Sep	1	10	1	10	1	10
2000	Oct	1	10	1	10	1	10
2000	Nov	1	10	1	10	1	10
2000	Dec	1	10	1	10	1	10

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tacatgtcag	aaaataagg	agttcctctg	catgggggtg	atgaagacag	550
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gatatcggt	atgtcgacac	cacccactgg	aaggtctacg	ttatagccag	1150

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val
 50 55 60
 Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala
 65 70 75
 Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val
 80 85 90
 Leu Ser Gly Ala His Thr Trp Arg Ser Leu Ile His His Ile Arg
 95 100 105
 Leu Met Ser Leu Pro Ile Ala Lys Lys Tyr Met Ser Glu Asn Lys
 110 115 120
 Gly Val Pro Leu His Gly Gly Asp Glu Asp Arg Pro Phe Pro Asp
 125 130 135
 Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu
 140 145 150
 Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys
 155 160 165
 Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His
 170 175 180
 Pro Leu Val Ile Lys Thr Gly Lys Pro Leu Leu Glu Glu Glu Ile
 185 190 195
 Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser
 200 205 210
 Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp
 215 220 225
 Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln
 230 235 240
 Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro
 245 250 255

Lys	Asp	Ala	Ser	Leu	Asn	Lys	Cys	Ser	Phe	Leu	His	Pro	Glu	Pro
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Val	Val	Gly	Ser	Lys	Met	His	Lys	Met	Pro	Asp	Leu	Phe	Ile	Ile
				275					280					285
Gly	Ser	Gly	Glu	Ala	Met	Leu	Gln	Leu	Ile	Pro	Pro	Phe	Gln	Cys
				290					295					300
Arg	Arg	His	Cys	Gln	Ser	Val	Ala	Met	Pro	Ile	Glu	Pro	Gly	Asp
				305					310					315
Ile	Gly	Tyr	Val	Asp	Thr	Thr	His	Trp	Lys	Val	Tyr	Val	Ile	Ala
				320					325					330
Arg	Gly	Val	Gln	Pro	Leu	Val	Ile	Cys	Asp	Gly	Thr	Ala	Phe	Ser
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Glu Leu

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 <212> DNA
 <213> Homo sapiens

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<210> 32
 <211> 3531
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Gln Glu Leu Val Leu Glu Pro Ala Gln Arg Arg Ala Arg Leu Glu
 50 55 60
 Gly Leu Arg Tyr Thr Ala Val Leu Lys Gln Gln Ala Thr Gln His
 65 70 75
 Ser Met Ala Leu Leu His Trp Gly Ala Leu Trp Arg Gln Leu Ala
 80 85 90
 Ser Pro Cys Gly Ala Trp Ala Leu Arg Asp Thr Pro Ile Pro Arg
 95 100 105
 Trp Lys Leu Ser Ser Ala Glu Thr Tyr Ser Arg Met Arg Leu Lys
 110 115 120
 Leu Val Pro Asn His His Phe Asp Pro His Leu Glu Ala Ser Ala
 125 130 135
 Leu Arg Asp Asn Leu Gly Glu Val Pro Leu Thr Pro Thr Glu Glu
 140 145 150
 Ala Ser Leu Pro Leu Ala Val Thr Lys Glu Ala Lys Val Ser Thr
 155 160 165
 Pro Pro Glu Leu Leu Gln Glu Asp Gln Leu Gly Glu Asp Glu Leu
 170 175 180
 Ala Glu Leu Glu Thr Pro Met Glu Ala Ala Glu Leu Asp Glu Gln
 185 190 195
 Arg Glu Lys Leu Val Leu Ser Ala Glu Cys Gln Leu Val Thr Val
 200 205 210
 Val Ala Val Val Pro Gly Leu Leu Glu Val Thr Thr Gln Asn Val
 215 220 225
 Tyr Phe Tyr Asp Gly Ser Thr Glu Arg Val Glu Thr Glu Glu Gly
 230 235 240
 Ile Gly Tyr Asp Phe Arg Arg Pro Leu Ala Gln Leu Arg Glu Val
 245 250 255
 His Leu Arg Arg Phe Asn Leu Arg Arg Ser Ala Leu Glu Leu Phe
 260 265 270

Phe Ile Asp Gln	Ala Asn Tyr Phe Leu	Asn Phe Pro Cys Lys	Val
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Gly Thr Thr Pro	Val Ser Ser Pro Ser	Gln Thr Pro Arg Pro	Gln
	290	295	300
Pro Gly Pro Ile	Pro Pro His Thr Gln	Val Arg Asn Gln Val	Tyr
	305	310	315
Ser Trp Leu Leu	Arg Leu Arg Pro Pro	Ser Gln Gly Tyr Leu	Ser
	320	325	330
Ser Arg Ser Pro	Gln Glu Met Leu Arg	Ala Ser Gly Leu Thr	Gln
	335	340	345
Lys Trp Val Gln	Arg Glu Ile Ser Asn	Phe Glu Tyr Leu Met	Gln
	350	355	360
Leu Asn Thr Ile	Ala Gly Arg Thr Tyr	Asn Asp Leu Ser Gln	Tyr
	365	370	375
Pro Val Phe Pro	Trp Val Leu Gln Asp	Tyr Val Ser Pro Thr	Leu
	380	385	390
Asp Leu Ser Asn	Pro Ala Val Phe Arg	Asp Leu Ser Lys Pro	Ile
	395	400	405
Gly Val Val Asn	Pro Lys His Ala Gln	Leu Val Arg Glu Lys	Tyr
	410	415	420
Glu Ser Phe Glu	Asp Pro Ala Gly Thr	Ile Asp Lys Phe His	Tyr
	425	430	435
Gly Thr His Tyr	Ser Asn Ala Ala Gly	Val Met His Tyr Leu	Ile
	440	445	450
Arg Val Glu Pro	Phe Thr Ser Leu His	Val Gln Leu Gln Ser	Gly
	455	460	465
Arg Phe Asp Cys	Ser Asp Arg Gln Phe	His Ser Val Ala Ala	Ala
	470	475	480
Trp Gln Ala Arg	Leu Glu Ser Pro Ala	Asp Val Lys Glu Leu	Ile
	485	490	495
Pro Glu Phe Phe	Tyr Phe Pro Asp Phe	Leu Glu Asn Gln Asn	Gly
	500	505	510
Phe Asp Leu Gly	Cys Leu Gln Leu Thr	Asn Glu Lys Val Gly	Asp
	515	520	525
Val Val Leu Pro	Pro Trp Ala Ser Ser	Pro Glu Asp Phe Ile	Gln
	530	535	540
Gln His Arg Gln	Ala Leu Glu Ser Glu	Tyr Val Ser Ala His	Leu
	545	550	555
His Glu Trp Ile	Asp Leu Ile Phe Gly	Tyr Lys Gln Arg Gly	Pro
	560	565	570
Ala Ala Glu Glu	Ala Leu Asn Val Phe	Tyr Tyr Cys Thr Tyr	Glu
	575	580	585

Gly	Ala	Val	Asp	Leu 590	Asp	His	Val	Thr	Asp 595	Glu	Arg	Glu	Arg	Lys 600
Ala	Leu	Glu	Gly	Ile 605	Ile	Ser	Asn	Phe	Gly 610	Gln	Thr	Pro	Cys	Gln 615
Leu	Leu	Lys	Glu	Pro 620	His	Pro	Thr	Arg	Leu 625	Ser	Ala	Glu	Glu	Ala 630
Ala	His	Arg	Leu	Ala 635	Arg	Leu	Asp	Thr	Asn 640	Ser	Pro	Ser	Ile	Phe 645
Gln	His	Leu	Asp	Glu 650	Leu	Lys	Ala	Phe	Phe 655	Ala	Glu	Val	Thr	Val 660
Ser	Ala	Ser	Gly	Leu 665	Leu	Gly	Thr	His	Ser 670	Trp	Leu	Pro	Tyr	Asp 675
Arg	Asn	Ile	Ser	Asn 680	Tyr	Phe	Ser	Phe	Ser 685	Lys	Asp	Pro	Thr	Met 690
Gly	Ser	His	Lys	Thr 695	Gln	Arg	Leu	Leu	Ser 700	Gly	Pro	Trp	Val	Pro 705
Gly	Ser	Gly	Val	Ser 710	Gly	Gln	Ala	Leu	Ala 715	Val	Ala	Pro	Asp	Gly 720
Lys	Leu	Leu	Phe	Ser 725	Gly	Gly	His	Trp	Asp 730	Gly	Ser	Leu	Arg	Val 735
Thr	Ala	Leu	Pro	Arg 740	Gly	Lys	Leu	Leu	Ser 745	Gln	Leu	Ser	Cys	His 750
Leu	Asp	Val	Val	Thr 755	Cys	Leu	Ala	Leu	Asp 760	Thr	Cys	Gly	Ile	Tyr 765
Leu	Ile	Ser	Gly	Ser 770	Arg	Asp	Thr	Thr	Cys 775	Met	Val	Trp	Arg	Leu 780
Leu	His	Gln	Gly	Gly 785	Leu	Ser	Val	Gly	Leu 790	Ala	Pro	Lys	Pro	Val 795
Gln	Val	Leu	Tyr	Gly 800	His	Gly	Ala	Ala	Val 805	Ser	Cys	Val	Ala	Ile 810
Ser	Thr	Glu	Leu	Asp 815	Met	Ala	Val	Ser	Gly 820	Ser	Glu	Asp	Gly	Thr 825
Val	Ile	Ile	His	Thr 830	Val	Arg	Arg	Gly	Gln 835	Phe	Val	Ala	Ala	Leu 840
Arg	Pro	Leu	Gly	Ala 845	Thr	Phe	Pro	Gly	Pro 850	Ile	Phe	His	Leu	Ala 855
Leu	Gly	Ser	Glu	Gly 860	Gln	Ile	Val	Val	Gln 865	Ser	Ser	Ala	Trp	Glu 870
Arg	Pro	Gly	Ala	Gln 875	Val	Thr	Tyr	Ser	Leu 880	His	Leu	Tyr	Ser	Val 885
Asn	Gly	Lys	Leu	Arg 890	Ala	Ser	Leu	Pro	Leu 895	Ala	Glu	Gln	Pro	Thr 900

Lys	Leu	Arg	Gly	Val	Gln	Asn	Pro	Val	Ala	Arg	Cys	Ile	Met	Cys	
				140					145					150	
Cys	Phe	Lys	Cys	Cys	Leu	Trp	Cys	Leu	Glu	Lys	Phe	Ile	Lys	Phe	
				155					160					165	
Leu	Asn	Arg	Asn	Ala	Tyr	Ile	Met	Ile	Ala	Ile	Tyr	Gly	Lys	Asn	
				170					175					180	
Phe	Cys	Val	Ser	Ala	Lys	Asn	Ala	Phe	Met	Leu	Leu	Met	Arg	Asn	
				185					190					195	
Ile	Val	Arg	Val	Val	Val	Leu	Asp	Lys	Val	Thr	Asp	Leu	Leu	Leu	
				200					205					210	
Phe	Phe	Gly	Lys	Leu	Leu	Val	Val	Gly	Gly	Val	Gly	Val	Leu	Ser	
				215					220					225	
Phe	Phe	Phe	Phe	Ser	Gly	Arg	Ile	Pro	Gly	Leu	Gly	Lys	Asp	Phe	
				230					235					240	
Lys	Ser	Pro	His	Leu	Asn	Tyr	Tyr	Trp	Leu	Pro	Ile	Met	Thr	Ser	
				245					250					255	
Ile	Leu	Gly	Ala	Tyr	Val	Ile	Ala	Ser	Gly	Phe	Phe	Ser	Val	Phe	
				260					265					270	
Gly	Met	Cys	Val	Asp	Thr	Leu	Phe	Leu	Cys	Phe	Leu	Glu	Asp	Leu	
				275					280					285	
Glu	Arg	Asn	Asn	Gly	Ser	Leu	Asp	Arg	Pro	Tyr	Tyr	Met	Ser	Lys	
				290					295					300	
Ser	Leu	Leu	Lys	Ile	Leu	Gly	Lys	Lys	Asn	Glu	Ala	Pro	Pro	Asp	
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Asn	Lys	Lys	Arg	Lys	Lys										
				320											

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 37
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<210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 38
 gtctttaccc agccccggga tgcg 24

<210> 39
 <211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
ggcctaattcc aacgtttctgt cttcaatctg caaatctatg gggtcctggg 50

<210> 40
<211> 1365
<212> DNA
<213> Homo sapiens

<400> 40
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aggtgggtcca gagccagagg gtccttctct tcgtggcctc ggacgtggat 150
gctctgtgtg cgtgcaagat ccttcaggcc ttgttccagt gtgaccacgt 200
gcaatatacg ctggttcag tttctgggtg gcaagaactt gaaactgcat 250
ttcttgagca taaagaacag tttcattatt ttattctcat aaactgtgga 300
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gcctatgaag acatcttcag ggatgaagag gaggatgaag agcattcagg 500
aaatgacagt gatgggtcag agccttctga gaagcgaca cggttagaag 550
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 accattgcca gctgc 1365

<210> 41

<211> 566

<212> PRT

<213> Homo sapiens

<400> 41

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				20					25					30
Cys	Ala	Cys	Lys	Ile	Leu	Gln	Ala	Leu	Phe	Gln	Cys	Asp	His	Val
				35					40					45
Gln	Tyr	Thr	Leu	Val	Pro	Val	Ser	Gly	Trp	Gln	Glu	Leu	Glu	Thr
				50					55					60
Ala	Phe	Leu	Glu	His	Lys	Glu	Gln	Phe	His	Tyr	Phe	Ile	Leu	Ile
				65					70					75
Asn	Cys	Gly	Ala	Asn	Val	Asp	Leu	Leu	Asp	Ile	Leu	Gln	Pro	Asp
				80					85					90
Glu	Asp	Thr	Ile	Phe	Phe	Val	Cys	Asp	Ser	His	Arg	Pro	Val	Asn
				95					100					105
Val	Val	Asn	Val	Tyr	Asn	Asp	Thr	Gln	Ile	Lys	Leu	Leu	Ile	Lys
				110					115					120
Gln	Asp	Asp	Asp	Leu	Glu	Val	Pro	Ala	Tyr	Glu	Asp	Ile	Phe	Arg
				125					130					135
Asp	Glu	Glu	Glu	Asp	Glu	Glu	His	Ser	Gly	Asn	Asp	Ser	Asp	Gly
				140					145					150
Ser	Glu	Pro	Ser	Glu	Lys	Arg	Thr	Arg	Leu	Glu	Glu	Glu	Ile	Val
				155					160					165
Glu	Gln	Thr	Met	Arg	Arg	Arg	Gln	Arg	Arg	Glu	Trp	Glu	Ala	Arg
				170					175					180
Arg	Arg	Asp	Ile	Leu	Phe	Asp	Tyr	Glu	Gln	Tyr	Glu	Tyr	His	Gly
				185					190					195
Thr	Ser	Ser	Ala	Met	Val	Met	Phe	Glu	Leu	Ala	Trp	Met	Leu	Ser
				200					205					210
Lys	Asp	Leu	Asn	Asp	Met	Leu	Trp	Trp	Ala	Ile	Val	Gly	Leu	Thr
				215					220					225
Asp	Gln	Trp	Val	Gln	Asp	Lys	Ile	Thr	Gln	Met	Lys	Tyr	Val	Thr
				230					235					240
Asp	Val	Gly	Val	Leu	Gln	Arg	His	Val	Ser	Arg	His	Asn	His	Arg

<210> 42
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 44, 118, 172, 183
 <223> unknown base

<400> 42
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 ccgatttccg caaagagttc tacgaggtgg tccagagcca gagggtcctt 100
 ctcttcgtgg cctcggangt ggatgctctg tgtgcgtgca agatccttca 150
 ggccttggtc cagtgtgacc angtgcaata tangctgggt ccagtttctg 200
 ggtggcaaga acttgaaact gcatttcttg agcataaaga acagtttcat 250
 tattttattc tcataaactg tggagctaata gtagacctat tggatattct 300
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 tcaatgttgt caatgtatac aacgataccc 380

<210> 43
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 43
 ttccgcaaag agttctacga ggtgg 25

<210> 44
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 44
 attgacaaca ttgactggcc tatggg 26

<210> 45
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 45
 gtggatgctc tgtgtgcgtg caagatcctt caggccttgt tocagtgtga 50

<210> 46

<211> 3089
<212> DNA
<213> Homo sapiens

<400> 46

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aggaacgaaa agagacagtt ttttttggaa agctaagtct tccctttatc 200
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taaagaatgc tgtctcctct tggaaaaaaaa aaaaaaaaaa 3089

<210> 47
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> Signal Peptide
<222> 1-20
<223> Signal Peptide

<220>
<221> N-glycosylation Site
<222> 72-75
<223> N-glycosylation Site

<220>
<221> Clq Domain Proteins
<222> 144-178, 78-111, 84-117
<223> Clq Domain Proteins

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35 40 45
Pro Leu Asp Pro Ala His Val Ser Ser Ala Ser Ser Ser Gly Arg
50 55 60
Pro His Ala Leu Pro Glu Ile Arg Pro Tyr Ile Asn Ile Thr Ile
65 70 75
Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met Gly Leu Pro Gly
80 85 90
Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly Pro Gln Gly
95 100 105
Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala Pro Cys
110 115 120
Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala Leu
125 130 135
His Ser Gly Glu Asp Phe Gln Thr Leu Leu Phe Glu Arg Val Phe
140 145 150
Val Asn Leu Asp Gly Cys Phe Asp Met Ala Thr Gly Gln Phe Ala
155 160 165
Ala Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser
170 175 180
Trp Asn Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys
185 190 195
Glu Ala Val Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met

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Gln Ser Gln Ser Val Met Leu Asp Leu	Ala Tyr Gly Asp Arg Val				
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Trp Val Arg Leu Phe Lys Arg Gln Arg	Glu Asn Ala Ile Tyr Ser				
230	235				240
Asn Asp Phe Asp Thr Tyr Ile Thr Phe	Ser Gly His Leu Ile Lys				
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Ala Glu Asp Asp					

<210> 48
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 48
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<210> 49
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 49
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<210> 50
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 50
 ctacttcttc agcctcaatg tgcacagctg gaattacaag gagacgtacg 50

<210> 51
 <211> 2768
 <212> DNA
 <213> Homo sapiens

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 ccgcctcccg ggacagaaga tgtgctccag ggtccctctg ctgctgccgc 150
 tgctcctgct actggccctg gggcctggg tgcagggctg cccatccggc 200
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<223> Synthetic oligonucleotide probe

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<210> 57

<211> 811

<212> PRT

<213> Homo sapiens

<400> 57

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Thr	Ala	Glu	Gly	Asp	Ala	Pro	Glu	Leu	Pro	Glu	Glu	Arg	Glu	Leu
				20					25					30

Met	Thr	Asn	Cys	Ser	Asn	Met	Ser	Leu	Arg	Lys	Val	Pro	Ala	Asp
				35					40					45

Leu	Thr	Pro	Ala	Thr	Thr	Thr	Leu	Asp	Leu	Ser	Tyr	Asn	Leu	Leu
				50					55					60

Phe	Gln	Leu	Gln	Ser	Ser	Asp	Phe	His	Ser	Val	Ser	Lys	Leu	Arg
				65					70					75

Val	Leu	Ile	Leu	Cys	His	Asn	Arg	Ile	Gln	Gln	Leu	Asp	Leu	Lys
				80					85					90

Thr Phe Glu Phe Asn Lys Glu Leu Arg Tyr Leu Asp Leu Ser Asn	95	100	105
Asn Arg Leu Lys Ser Val Thr Trp Tyr Leu Leu Ala Gly Leu Arg	110	115	120
Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp Thr Met Pro Ile Cys	125	130	135
Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile Leu Gly Leu Ser	140	145	150
Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln Lys Ile Ala His Leu	155	160	165
His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro His Tyr	170	175	180
Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His Ile	185	190	195
Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg Asp Gly	200	205	210
Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys	215	220	225
Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu	230	235	240
Asn Ala Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu	245	250	255
Trp Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser	260	265	270
Val Glu His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala	275	280	285
Tyr Leu Asp His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg	290	295	300
Thr Ile Lys Leu Glu His Val His Phe Arg Val Phe Tyr Ile Gln	305	310	315
Gln Asp Lys Ile Tyr Leu Leu Leu Thr Lys Met Asp Ile Glu Asn	320	325	330
Leu Thr Ile Ser Asn Ala Gln Met Pro His Met Leu Phe Pro Asn	335	340	345
Tyr Pro Thr Lys Phe Gln Tyr Leu Asn Phe Ala Asn Asn Ile Leu	350	355	360
Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln Leu Pro His Leu Lys	365	370	375
Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr Leu Ser Leu Val	380	385	390
Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu Asp Leu Ser	395	400	405

Gln	Asn	Leu	Leu	Gln	His	Lys	Asn	Asp	Glu	Asn	Cys	Ser	Trp	Pro
				410					415					420
Glu	Thr	Val	Val	Asn	Met	Asn	Leu	Ser	Tyr	Asn	Lys	Leu	Ser	Asp
				425					430					435
Ser	Val	Phe	Arg	Cys	Leu	Pro	Lys	Ser	Ile	Gln	Ile	Leu	Asp	Leu
				440					445					450
Asn	Asn	Asn	Gln	Ile	Gln	Thr	Val	Pro	Lys	Glu	Thr	Ile	His	Leu
				455					460					465
Met	Ala	Leu	Arg	Glu	Leu	Asn	Ile	Ala	Phe	Asn	Phe	Leu	Thr	Asp
				470					475					480
Leu	Pro	Gly	Cys	Ser	His	Phe	Ser	Arg	Leu	Ser	Val	Leu	Asn	Ile
				485					490					495
Glu	Met	Asn	Phe	Ile	Leu	Ser	Pro	Ser	Leu	Asp	Phe	Val	Gln	Ser
				500					505					510
Cys	Gln	Glu	Val	Lys	Thr	Leu	Asn	Ala	Gly	Arg	Asn	Pro	Phe	Arg
				515					520					525
Cys	Thr	Cys	Glu	Leu	Lys	Asn	Phe	Ile	Gln	Leu	Glu	Thr	Tyr	Ser
				530					535					540
Glu	Val	Met	Met	Val	Gly	Trp	Ser	Asp	Ser	Tyr	Thr	Cys	Glu	Tyr
				545					550					555
Pro	Leu	Asn	Leu	Arg	Gly	Thr	Arg	Leu	Lys	Asp	Val	His	Leu	His
				560					565					570
Glu	Leu	Ser	Cys	Asn	Thr	Ala	Leu	Leu	Ile	Val	Thr	Ile	Val	Val
				575					580					585
Ile	Met	Leu	Val	Leu	Gly	Leu	Ala	Val	Ala	Phe	Cys	Cys	Leu	His
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Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Leu	Gly	Gln	Cys	Thr	Gln
				605					610					615
Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr	Gln	Glu	Gln	Leu	Lys	Arg
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Asn	Val	Arg	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	His	Asp	Ser
				635					640					645
Leu	Trp	Val	Lys	Asn	Glu	Leu	Ile	Pro	Asn	Leu	Glu	Lys	Glu	Asp
				650					655					660
Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe	Asp	Pro	Gly
				665					670					675
Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys	Ser	Tyr
				680					685					690
Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu	Trp
				695					700					705
Cys	His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu
				710					715					720

Asn	Ser	Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe
				725					730					735
Tyr	Cys	Ile	Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu
				740					745					750
Lys	Lys	Ala	Tyr	Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly
				755					760					765
Leu	Phe	Trp	Ala	Asn	Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu
				770					775					780
Ala	Thr	Arg	Glu	Met	Tyr	Glu	Leu	Gln	Thr	Phe	Thr	Glu	Leu	Asn
				785					790					795
Glu	Glu	Ser	Arg	Gly	Ser	Thr	Ile	Ser	Leu	Met	Arg	Thr	Asp	Cys
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Leu

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 58
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<210> 59
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<210> 61
 <211> 3772
 <212> DNA
 <213> Homo sapiens

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<211> 756

<212> PRT

<213> Homo sapiens

<400> 62

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Glu	Asp	Pro	Asp	Tyr	Tyr	Gly	Gln	Glu	Ile	Trp	Ser	Arg	Glu	Pro	35	40	45	
Tyr	Tyr	Ala	Arg	Pro	Glu	Pro	Glu	Leu	Glu	Thr	Phe	Ser	Pro	Pro	50	55	60	
Leu	Pro	Ala	Gly	Pro	Gly	Glu	Glu	Trp	Glu	Arg	Arg	Pro	Gln	Glu	65	70	75	
Pro	Arg	Pro	Pro	Lys	Arg	Ala	Thr	Lys	Pro	Lys	Lys	Ala	Pro	Lys	80	85	90	
Arg	Glu	Lys	Ser	Ala	Pro	Glu	Pro	Pro	Pro	Pro	Gly	Lys	His	Ser	95	100	105	
Asn	Lys	Lys	Val	Met	Arg	Thr	Lys	Ser	Ser	Glu	Lys	Ala	Ala	Asn	110	115	120	
Asp	Asp	His	Ser	Val	Arg	Val	Ala	Arg	Glu	Asp	Val	Arg	Glu	Ser	125	130	135	
Cys	Pro	Pro	Leu	Gly	Leu	Glu	Thr	Leu	Lys	Ile	Thr	Asp	Phe	Gln	140	145	150	
Leu	His	Ala	Ser	Thr	Val	Lys	Arg	Tyr	Gly	Leu	Gly	Ala	His	Arg	155	160	165	
Gly	Arg	Leu	Asn	Ile	Gln	Ala	Gly	Ile	Asn	Glu	Asn	Asp	Phe	Tyr	170	175	180	
Asp	Gly	Ala	Trp	Cys	Ala	Gly	Arg	Asn	Asp	Leu	Gln	Gln	Trp	Ile				

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Gln Gly Arg Asn	Ser Leu Trp Leu Ser	Asp Trp Val Thr Ser	Tyr
	215	220	225
Lys Val Met Val	Ser Asn Asp Ser His	Thr Trp Val Thr Val	Lys
	230	235	240
Asn Gly Ser Gly	Asp Met Ile Phe Glu	Gly Asn Ser Glu Lys	Glu
	245	250	255
Ile Pro Val Leu	Asn Glu Leu Pro Val	Pro Met Val Ala Arg	Tyr
	260	265	270
Ile Arg Ile Asn	Pro Gln Ser Trp Phe	Asp Asn Gly Ser Ile	Cys
	275	280	285
Met Arg Met Glu	Ile Leu Gly Cys Pro	Leu Pro Asp Pro Asn	Asn
	290	295	300
Tyr Tyr His Arg	Arg Asn Glu Met Thr	Thr Thr Asp Asp Leu	Asp
	305	310	315
Phe Lys His His	Asn Tyr Lys Glu Met	Arg Gln Leu Met Lys	Val
	320	325	330
Val Asn Glu Met	Cys Pro Asn Ile Thr	Arg Ile Tyr Asn Ile	Gly
	335	340	345
Lys Ser His Gln	Gly Leu Lys Leu Tyr	Ala Val Glu Ile Ser	Asp
	350	355	360
His Pro Gly Glu	His Glu Val Gly Glu	Pro Glu Phe His Tyr	Ile
	365	370	375
Ala Gly Ala His	Gly Asn Glu Val Leu	Gly Arg Glu Leu Leu	Leu
	380	385	390
Leu Leu Val Gln	Phe Val Cys Gln Glu	Tyr Leu Ala Arg Asn	Ala
	395	400	405
Arg Ile Val His	Leu Val Glu Glu Thr	Arg Ile His Val Leu	Pro
	410	415	420
Ser Leu Asn Pro	Asp Gly Tyr Glu Lys	Ala Tyr Glu Gly Gly	Ser
	425	430	435
Glu Leu Gly Gly	Trp Ser Leu Gly Arg	Trp Thr His Asp Gly	Ile
	440	445	450
Asp Ile Asn Asn	Asn Phe Pro Asp Leu	Asn Thr Leu Leu Trp	Glu
	455	460	465
Ala Glu Asp Arg	Gln Asn Val Pro Arg	Lys Val Pro Asn His	Tyr
	470	475	480
Ile Ala Ile Pro	Glu Trp Phe Leu Ser	Glu Asn Ala Thr Val	Ala
	485	490	495
Ala Glu Thr Arg	Ala Val Ile Ala Trp	Met Glu Lys Ile Pro	Phe

500	505	510
Val Leu Gly Gly Asn Leu Gln Gly Gly	Glu Leu Val Val Ala Tyr	
515	520	525
Pro Tyr Asp Leu Val Arg Ser Pro Trp	Lys Thr Gln Glu His Thr	
530	535	540
Pro Thr Pro Asp Asp His Val Phe Arg	Trp Leu Ala Tyr Ser Tyr	
545	550	555
Ala Ser Thr His Arg Leu Met Thr Asp	Ala Arg Arg Arg Val Cys	
560	565	570
His Thr Glu Asp Phe Gln Lys Glu Glu	Gly Thr Val Asn Gly Ala	
575	580	585
Ser Trp His Thr Val Ala Gly Ser Leu	Asn Asp Phe Ser Tyr Leu	
590	595	600
His Thr Asn Cys Phe Glu Leu Ser Ile	Tyr Val Gly Cys Asp Lys	
605	610	615
Tyr Pro His Glu Ser Gln Leu Pro Glu	Glu Trp Glu Asn Asn Arg	
620	625	630
Glu Ser Leu Ile Val Phe Met Glu Gln	Val His Arg Gly Ile Lys	
635	640	645
Gly Leu Val Arg Asp Ser His Gly Lys	Gly Ile Pro Asn Ala Ile	
650	655	660
Ile Ser Val Glu Gly Ile Asn His Asp	Ile Arg Thr Ala Asn Asp	
665	670	675
Gly Asp Tyr Trp Arg Leu Leu Asn Pro	Gly Glu Tyr Val Val Thr	
680	685	690
Ala Lys Ala Glu Gly Phe Thr Ala Ser	Thr Lys Asn Cys Met Val	
695	700	705
Gly Tyr Asp Met Gly Ala Thr Arg Cys	Asp Phe Thr Leu Ser Lys	
710	715	720
Thr Asn Met Ala Arg Ile Arg Glu Ile	Met Glu Lys Phe Gly Lys	
725	730	735
Gln Pro Val Ser Leu Pro Ala Arg Arg	Leu Lys Leu Arg Gly Arg	
740	745	750
Lys Arg Arg Gln Arg Gly		
755		

<210> 63
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 63
 gttctcaatg agctaccggt cccc 24

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 64
cgcgatgtag tggaaactcgg gctc 24

<210> 65
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
atccgcataa accctcagtc ctggtttgat aatgggagca tctgcatgag 50

<210> 66
<211> 2854
<212> DNA
<213> Homo sapiens

<400> 66
ctaagaggac aagatgaggc cgggcctctc atttctccta gcccttctgt 50
tcttccttgg ccaagctgca ggggatttgg gggatgtggg acctccaatt 100
cccagccccg gcttcagctc tttcccaggt gttgactcca gctccagctt 150
cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200
gaggttctgt gtcccagttg ttttccaatt tcaccggctc cgtggatgac 250
cgtgggacct gccagtgtc tgtttccctg ccagacacca cctttcccgt 300
ggacagagtg gaacgcttgg aattcacagc tcatgttctt tctcagaagt 350
ttgagaaaga actttctaaa gtgaggaat atgtccaatt aattagtgtg 400
tatgaaaaga aactgttaaa cctaactgtc cgaattgaca tcatggagaa 450
ggataccatt tcttacctg aactggactt cgagctgac aaggtagaag 500
tgaaggagat ggaaaaactg gtcatacagc tgaaggagag ttttggtgga 550
agctcagaaa ttgttgacca gctggaggtg gagataagaa atatgactct 600
cttggtagag aagcttgaga cactagacaa aaacaatgtc cttgccattc 650
gccgagaaat cgtggctctg aagaccaagc tgaaagagtg tgaggcctct 700
aaagatcaaa acaccctgt cgtccaccct cctccactc caggagctg 750
tggtcatggt ggtgtggtga acatcagcaa accgtctgtg gttcagctca 800
actggagagg gttttcttat ctatatggtg cttggggtag ggattactct 850
ccccagcatc caaacaagg actgtattgg gtggcgccat tgaatacaga 900

aagaccttgg agcatatgtg caacttatga gtgtatcagt tgttgcatgt 2550
aatttttggc tttgtttaag cctggaactt gtaagaaaat gaaaatttaa 2600
tttttttttc taggacgagc tatagaaaag ctattgagag tatctagtta 2650
atcagtgcag tagttggaaa ccttgctggt gtatgtgatg tgcttctgtg 2700
cttttgaatg actttatcat ctagtctttg tctatttttc ctttgatgtt 2750
caagtcctag tctataggat tggcagttta aatgctttac tccccctttt 2800
aaaataaatg attaaaatgt gctttgaaaa aaaaaaaaaa aaaaaaaaaa 2850
aaaa 2854

<210> 67
<211> 510
<212> PRT
<213> Homo sapiens

<400> 67
Met Arg Pro Gly Leu Ser Phe Leu Leu Ala Leu Leu Phe Phe Leu
1 5 10 15
Gly Gln Ala Ala Gly Asp Leu Gly Asp Val Gly Pro Pro Ile Pro
20 25 30
Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser
35 40 45
Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Ser Arg Ser Leu
50 55 60
Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly
65 70 75
Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu Pro
80 85 90
Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr
95 100 105
Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val
110 115 120
Arg Glu Tyr Val Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu
125 130 135
Asn Leu Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser
140 145 150
Tyr Thr Glu Leu Asp Phe Glu Leu Ile Lys Val Glu Val Lys Glu
155 160 165
Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser
170 175 180
Ser Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr
185 190 195
Leu Leu Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu
200 205 210

Ala	Ile	Arg	Arg	Glu	Ile	Val	Ala	Leu	Lys	Thr	Lys	Leu	Lys	Glu	215	220	225
Cys	Glu	Ala	Ser	Lys	Asp	Gln	Asn	Thr	Pro	Val	Val	His	Pro	Pro	230	235	240
Pro	Thr	Pro	Gly	Ser	Cys	Gly	His	Gly	Gly	Val	Val	Asn	Ile	Ser	245	250	255
Lys	Pro	Ser	Val	Val	Gln	Leu	Asn	Trp	Arg	Gly	Phe	Ser	Tyr	Leu	260	265	270
Tyr	Gly	Ala	Trp	Gly	Arg	Asp	Tyr	Ser	Pro	Gln	His	Pro	Asn	Lys	275	280	285
Gly	Leu	Tyr	Trp	Val	Ala	Pro	Leu	Asn	Thr	Asp	Gly	Arg	Leu	Leu	290	295	300
Glu	Tyr	Tyr	Arg	Leu	Tyr	Asn	Thr	Leu	Asp	Asp	Leu	Leu	Leu	Tyr	305	310	315
Ile	Asn	Ala	Arg	Glu	Leu	Arg	Ile	Thr	Tyr	Gly	Gln	Gly	Ser	Gly	320	325	330
Thr	Ala	Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn	Met	Tyr	Asn	Thr	335	340	345
Gly	Asn	Ile	Ala	Arg	Val	Asn	Leu	Thr	Thr	Asn	Thr	Ile	Ala	Val	350	355	360
Thr	Gln	Thr	Leu	Pro	Asn	Ala	Ala	Tyr	Asn	Asn	Arg	Phe	Ser	Tyr	365	370	375
Ala	Asn	Val	Ala	Trp	Gln	Asp	Ile	Asp	Phe	Ala	Val	Asp	Glu	Asn	380	385	390
Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Ala	Ser	Thr	Gly	Asn	Met	395	400	405
Val	Ile	Ser	Lys	Leu	Asn	Asp	Thr	Thr	Leu	Gln	Val	Leu	Asn	Thr	410	415	420
Trp	Tyr	Thr	Lys	Gln	Tyr	Lys	Pro	Ser	Ala	Ser	Asn	Ala	Phe	Met	425	430	435
Val	Cys	Gly	Val	Leu	Tyr	Ala	Thr	Arg	Thr	Met	Asn	Thr	Arg	Thr	440	445	450
Glu	Glu	Ile	Phe	Tyr	Tyr	Tyr	Asp	Thr	Asn	Thr	Gly	Lys	Glu	Gly	455	460	465
Lys	Leu	Asp	Ile	Val	Met	His	Lys	Met	Gln	Glu	Lys	Val	Gln	Ser	470	475	480
Ile	Asn	Tyr	Asn	Pro	Phe	Asp	Gln	Lys	Leu	Tyr	Val	Tyr	Asn	Asp	485	490	495
Gly	Tyr	Leu	Leu	Asn	Tyr	Asp	Leu	Ser	Val	Leu	Gln	Lys	Pro	Gln	500	505	510

<210> 68
 <211> 410
 <212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 206, 217, 387

<223> unknown base

<400> 68

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cctgtcgtcc accctcctcc cactccaggg agctgtggtc atgggtggtgt 100
ggtgaacatc agcaaaccgt ctgtggttca gctcaactgg agaggggtttt 150
cttatctata tgggtgcttg ggtagggatt actctcccca gcatccaaac 200
aaaggnatgt attggngggc gccattgaat acagatggga gactgttgga 250
gtattataga ctgtacaacc cactggatga tttgctattg tatataaatg 300
ctcgagagtt gcggatcacc tatggccaag gtagtggtac agcagtttac 350
aacaacaaca tgtacgtcaa catgtacaac accgggnata ttgccagagt 400
taacctgacc 410

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 69

agctgtggtc atgggtggtgt ggtg 24

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ctaccttggc cataggtgat ccgc 24

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

catcagcaaa ccgtctgtgg ttcagctcaa ctggagaggg tt 42

<210> 72

<211> 3127

<212> DNA

<213> Homo sapiens

[illegible]

72

ttctccagtg ttctggcatg aattagattt tactgcttgt ctttttgta 1600
 ttttcttacc aagtgcattg atatgtgaag tagaatgaat tgcagaggaa 1650
 agttttatga atatggtgat gagttagtaa aagtggccat tattgggctt 1700
 attctctgct ctatagttgt gaaatgaaga gtaaaaacaa atttgtttga 1750
 ctattttaaa attatattag accttaagct gtttttagcaa gcattaaagc 1800
 aaatgtatgg ctgccttttg aaatatattga tgtgttgccct ggcaggatac 1850
 tgcaaagaac atgggtttatt ttaaaattta taaacaagtc acttaaagtc 1900
 cagttgtctg aaaaatctta taaggtttta cccttgatac ggaatttaca 1950
 caggtaggga gtgttttagtg gacaatagtg taggttatgg atggaggtgt 2000
 cgggtactaaa ttgaataacg agtaaataat cttacttggg tagagatggc 2050
 ctttgccaac aaagtgaact gttttgggtg ttttaaactc atgaagtatg 2100
 gggtcagtgg aaatgttttg aactctgaag gatttagaca aggttttgaa 2150
 aaggataatc atgggttaga aggaagtgtt ttgaaagtca ctttgaaagt 2200
 tagttttggg cccagcacgg tagctcacc ttggtaatcc cagcactttg 2250
 ggagcttaag tgggtagatt acttgagccc aggaattcag accagcttgg 2300
 cacatggtga acctgttcta taaaaataat ctggctttga gcatatgcct 2350
 gtggtccagc actgagaggc tagtgaagat tgctgagccc agagccaaag 2400
 gttgcagtga gcaagtcaag tcaactgcact ctagctggca cagagtaagc 2450
 caaaaaaata tatatatatt gaaatcaagg aggcaaaatt ttgacaggga 2500
 aggaagtaac tgcaaaacca ctaggcttta gtaggtactt atataaaatc 2550
 tagtccagtt ctctcattta aaaaatgaa gacactgaaa tacagactta 2600
 aatagctcag atagctaatt aggaaatttc aagttggcca ataatagcat 2650
 tctctctgac atttaaaaat aatttctatt caaaatacat gcatattgat 2700
 ttacacctca tactgtgata attaatgtga tgtggattgc tgggtgtccag 2750
 catgacccat aaacagggtca gaagaatgat ggaatgtttt agaataaaact 2800
 cctgcttata gtatactaca cagttcaaaa gatgtttaaa atgcttttgt 2850
 atttactgcc atgtaattga aatatataga ttattgtaac ctttcaacct 2900
 gaaaatcaag cagtatgaga gtttagttat ttgtatgtgt cactagtgtc 2950
 taatgaagct tttaaaatct acaatttctt ctttaaaaat atttattaat 3000
 gtgaatggaa tataacaatt cagcttaatt cccaacctt attctgtgtg 3050
 tagacattgt attccacaat tttgaatggc tgtgttttac ctctaaataa 3100
 atgaattcag agaaaaaaaa aaaaaaa 3127

<210> 73
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 73

Met	Gly	Ser	Val	Leu	Gly	Leu	Cys	Ser	Met	Ala	Ser	Trp	Ile	Pro
1				5					10					15
Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Leu	Leu	Cys	Arg	Cys	Cys	Pro
				20					25					30
Ser	Gly	Asn	Asn	Ser	Thr	Val	Thr	Arg	Leu	Ile	Tyr	Ala	Leu	Phe
				35					40					45
Leu	Leu	Val	Gly	Val	Cys	Val	Ala	Cys	Val	Met	Leu	Ile	Pro	Gly
				50					55					60
Met	Glu	Glu	Gln	Leu	Asn	Lys	Ile	Pro	Gly	Phe	Cys	Glu	Asn	Glu
				65					70					75
Lys	Gly	Val	Val	Pro	Cys	Asn	Ile	Leu	Val	Gly	Tyr	Lys	Ala	Val
				80					85					90
Tyr	Arg	Leu	Cys	Phe	Gly	Leu	Ala	Met	Phe	Tyr	Leu	Leu	Leu	Ser
				95					100					105
Leu	Leu	Met	Ile	Lys	Val	Lys	Ser	Ser	Ser	Asp	Pro	Arg	Ala	Ala
				110					115					120
Val	His	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Ala	Ala	Ala	Ile	Ala
				125					130					135
Ile	Ile	Ile	Gly	Ala	Phe	Phe	Ile	Pro	Glu	Gly	Thr	Phe	Thr	Thr
				140					145					150
Val	Trp	Phe	Tyr	Val	Gly	Met	Ala	Gly	Ala	Phe	Cys	Phe	Ile	Leu
				155					160					165
Ile	Gln	Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Glu
				170					175					180
Ser	Trp	Val	Glu	Lys	Met	Glu	Glu	Gly	Asn	Ser	Arg	Cys	Trp	Tyr
				185					190					195
Ala	Ala	Leu	Leu	Ser	Ala	Thr	Ala	Leu	Asn	Tyr	Leu	Leu	Ser	Leu
				200					205					210
Val	Ala	Ile	Val	Leu	Phe	Phe	Val	Tyr	Tyr	Thr	His	Pro	Ala	Ser
				215					220					225
Cys	Ser	Glu	Asn	Lys	Ala	Phe	Ile	Ser	Val	Asn	Met	Leu	Leu	Cys
				230					235					240
Val	Gly	Ala	Ser	Val	Met	Ser	Ile	Leu	Pro	Lys	Ile	Gln	Glu	Ser
				245					250					255
Gln	Pro	Arg	Ser	Gly	Leu	Leu	Gln	Ser	Ser	Val	Ile	Thr	Val	Tyr
				260					265					270
Thr	Met	Tyr	Leu	Thr	Trp	Ser	Ala	Met	Thr	Asn	Glu	Pro	Glu	Thr
				275					280					285

Asn	Cys	Asn	Pro	Ser	Leu	Leu	Ser	Ile	Ile	Gly	Tyr	Asn	Thr	Thr
				290					295					300
Ser	Thr	Val	Pro	Lys	Glu	Gly	Gln	Ser	Val	Gln	Trp	Trp	His	Ala
				305					310					315
Gln	Gly	Ile	Ile	Gly	Leu	Ile	Leu	Phe	Leu	Leu	Cys	Val	Phe	Tyr
				320					325					330
Ser	Ser	Ile	Arg	Thr	Ser	Asn	Asn	Ser	Gln	Val	Asn	Lys	Leu	Thr
				335					340					345
Leu	Thr	Ser	Asp	Glu	Ser	Thr	Leu	Ile	Glu	Asp	Gly	Gly	Ala	Arg
				350					355					360
Ser	Asp	Gly	Ser	Leu	Glu	Asp	Gly	Asp	Asp	Val	His	Arg	Ala	Val
				365					370					375
Asp	Asn	Glu	Arg	Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His
				380					385					390
Phe	Met	Leu	Phe	Leu	Ala	Ser	Leu	Tyr	Ile	Met	Met	Thr	Leu	Thr
				395					400					405
Asn	Trp	Ser	Arg	Tyr	Glu	Pro	Ser	Arg	Glu	Met	Lys	Ser	Gln	Trp
				410					415					420
Thr	Ala	Val	Trp	Val	Lys	Ile	Ser	Ser	Ser	Trp	Ile	Gly	Ile	Val
				425					430					435
Leu	Tyr	Val	Trp	Thr	Leu	Val	Ala	Pro	Leu	Val	Leu	Thr	Asn	Arg
				440					445					450

Asp Phe Asp

<210> 74
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 48, 163
 <223> unknown base

<400> 74
 gcgagaaaga agctgtctcc atcttgtctg tatcccgctg cttcttgnga 50
 cgttgtggag atggggagcg tccctggggc tgtgctccat ggcgagctgg 100
 ataccatgtt tgtgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150
 tagtggaac aantccactg taactagatt gatctatgca cttttcttgc 200
 ttgttgagat atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250
 caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300
 ttgtaacatt ttggttggtc ataaagctgt atatcgtttg tgctttggtt 350
 tggctatgtt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

agcagtgatc ctagagctgc agtgcacaat ggattttggt tctttaaatt 450
tgctgcagca attgcaatta ttattggggc 480

<210> 75

<211> 438

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323

<223> unknown base

<400> 75

gttattgtga actttgtgga gatgggaggt cntggggctg tgttccatgg 50
cgagctggat accangtttg tgtggaagtg ccccggtgtt gntatgccga 100
tgctgtccta gtggaacaa ntccactgta attagattga tntatgcact 150
ttntttgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200
tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250
gttgtccctt gtaacatttt ggttggctat aaagctgtat atngtttgtg 300
ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaag 350
tgaagagtag cagtgatcct agagctgcag tgcacaatgg attttggttt 400
tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76

<211> 473

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 48

<223> unknown base

<400> 76

aagaagctgt ctccatcttg tctgtatccg ctgctcttgt gaacgttntg 50
gagatgggga gcgtccttgg ggttgtgctc catggcgagc tggataccat 100
gtttgtgttg aagtgccccg tgtttgctat gccgatgctg tcctagtga 150
aacaactcca ctgtaactag attgatctat gcacttttct tgcttgttgg 200
agtatgtgta gotttgtgtaa tgttgatacc aggaatggaa gaacaactga 250
ataagattcc tggattttgt gagaatgaga aagggtgttg cccttgtaac 300
attttggttg gctataaagc tgtatatcgt ttgtgctttg gtttggctat 350
gttctatctt cttctctctt tactaatgat caaagtgaag agtagcagt 400
atcctagagc tgcagtgcac aatggatttt ggttctttaa atttgctgca 450
gcaattgcaa ttattattgg ggc 473

<210> 77
<211> 666
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 21, 111
<223> unknown base

<400> 77
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actttttcct tgcttggttg agtatgtgta gctttgtgta atgttggtcc 100
caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150
gaaagggtgtt gtccccttgt aacatttttg gttggctata aagctgtata 200
tcgtttgtgc tttggttttg ctatgttcta tcttcttctc tctttactaa 250
tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300
ttttggttct ttaaatttgc tgcagcaatt gcaattatta ttggggcatt 350
cttcattcca gaaggaaact ttacaactgt gtggttttat gtaggcatgg 400
cagggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450
gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaactc 500
gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550
tgtctttagt tgctatcgtc ctgttctttg tctactacac tcatccagcc 600
agttgttcag aaaacaaggc gttcatcagt gtcaacatgc tcctctgcgt 650
tggtgcttct gtaatg 666

<210> 78
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
atgtttgtgt ggaagtgccc cg 22

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
gtcaacatgc tcctctgc 18

<210> 80
<211> 26

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
aatccattgt gcaactgcagc tctagg 26

<210> 81
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
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<210> 82
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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gcac 54

<210> 83
<211> 3906
<212> DNA
<213> Homo sapiens

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 gaaaaa 3906

<210> 84
 <211> 867
 <212> PRT
 <213> Homo sapiens

<400> 84
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 35 40 45
 Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser
 50 55 60
 Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly
 65 70 75
 Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro
 80 85 90
 Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn
 95 100 105
 Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala
 110 115 120
 Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly
 125 130 135
 Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
 140 145 150
 Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys
 155 160 165
 Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys
 170 175 180
 Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu
 185 190 195
 Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met
 200 205 210
 Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro
 215 220 225
 His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
 230 235 240
 Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn
 245 250 255

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Ile	His	Met	Glu	Phe	Thr	Asn	Met	Leu	Gln	Arg	Lys	Arg	Leu	Gln
				275					280					285
Thr	Leu	Met	Ser	Val	Asp	Asp	Ser	Met	Glu	Thr	Ile	Tyr	Asn	Met
				290					295					300
Leu	Val	Glu	Thr	Gly	Glu	Leu	Asp	Asn	Thr	Tyr	Ile	Val	Tyr	Thr
				305					310					315
Ala	Asp	His	Gly	Tyr	His	Ile	Gly	Gln	Phe	Gly	Leu	Val	Lys	Gly
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Lys	Ser	Met	Pro	Tyr	Glu	Phe	Asp	Ile	Arg	Val	Pro	Phe	Tyr	Val
				335					340					345
Arg	Gly	Pro	Asn	Val	Glu	Ala	Gly	Cys	Leu	Asn	Pro	His	Ile	Val
				350					355					360
Leu	Asn	Ile	Asp	Leu	Ala	Pro	Thr	Ile	Leu	Asp	Ile	Ala	Gly	Leu
				365					370					375
Asp	Ile	Pro	Ala	Asp	Met	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Leu	Leu
				380					385					390
Asp	Thr	Glu	Arg	Pro	Val	Asn	Arg	Phe	His	Leu	Lys	Lys	Lys	Met
				395					400					405
Arg	Val	Trp	Arg	Asp	Ser	Phe	Leu	Val	Glu	Arg	Gly	Lys	Leu	Leu
				410					415					420
His	Lys	Arg	Asp	Asn	Asp	Lys	Val	Asp	Ala	Gln	Glu	Glu	Asn	Phe
				425					430					435
Leu	Pro	Lys	Tyr	Gln	Arg	Val	Lys	Asp	Leu	Cys	Gln	Arg	Ala	Glu
				440					445					450
Tyr	Gln	Thr	Ala	Cys	Glu	Gln	Leu	Gly	Gln	Lys	Trp	Gln	Cys	Val
				455					460					465
Glu	Asp	Ala	Thr	Gly	Lys	Leu	Lys	Leu	His	Lys	Cys	Lys	Gly	Pro
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Met	Arg	Leu	Gly	Gly	Ser	Arg	Ala	Leu	Ser	Asn	Leu	Val	Pro	Lys
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Tyr	Tyr	Gly	Gln	Gly	Ser	Glu	Ala	Cys	Thr	Cys	Asp	Ser	Gly	Asp
				500					505					510
Tyr	Lys	Leu	Ser	Leu	Ala	Gly	Arg	Arg	Lys	Lys	Leu	Phe	Lys	Lys
				515					520					525
Lys	Tyr	Lys	Ala	Ser	Tyr	Val	Arg	Ser	Arg	Ser	Ile	Arg	Ser	Val
				530					535					540
Ala	Ile	Glu	Val	Asp	Gly	Arg	Val	Tyr	His	Val	Gly	Leu	Gly	Asp
				545					550					555
Ala	Ala	Gln	Pro	Arg	Asn	Leu	Thr	Lys	Arg	His	Trp	Pro	Gly	Ala
				560					565					570

Pro	Glu	Asp	Gln	Asp	Asp	Lys	Asp	Gly	Gly	Asp	Phe	Ser	Gly	Thr	
				575					580					585	
Gly	Gly	Leu	Pro	Asp	Tyr	Ser	Ala	Ala	Asn	Pro	Ile	Lys	Val	Thr	
				590					595					600	
His	Arg	Cys	Tyr	Ile	Leu	Glu	Asn	Asp	Thr	Val	Gln	Cys	Asp	Leu	
				605					610					615	
Asp	Leu	Tyr	Lys	Ser	Leu	Gln	Ala	Trp	Lys	Asp	His	Lys	Leu	His	
				620					625					630	
Ile	Asp	His	Glu	Ile	Glu	Thr	Leu	Gln	Asn	Lys	Ile	Lys	Asn	Leu	
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Arg	Glu	Val	Arg	Gly	His	Leu	Lys	Lys	Lys	Arg	Pro	Glu	Glu	Cys	
				650					655					660	
Asp	Cys	His	Lys	Ile	Ser	Tyr	His	Thr	Gln	His	Lys	Gly	Arg	Leu	
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Lys	His	Arg	Gly	Ser	Ser	Leu	His	Pro	Phe	Arg	Lys	Gly	Leu	Gln	
				680					685					690	
Glu	Lys	Asp	Lys	Val	Trp	Leu	Leu	Arg	Glu	Gln	Lys	Arg	Lys	Lys	
				695					700					705	
Lys	Leu	Arg	Lys	Leu	Leu	Lys	Arg	Leu	Gln	Asn	Asn	Asp	Thr	Cys	
				710					715					720	
Ser	Met	Pro	Gly	Leu	Thr	Cys	Phe	Thr	His	Asp	Asn	Gln	His	Trp	
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Gln	Thr	Ala	Pro	Phe	Trp	Thr	Leu	Gly	Pro	Phe	Cys	Ala	Cys	Thr	
				740					745					750	
Ser	Ala	Asn	Asn	Asn	Thr	Tyr	Trp	Cys	Met	Arg	Thr	Ile	Asn	Glu	
				755					760					765	
Thr	His	Asn	Phe	Leu	Phe	Cys	Glu	Phe	Ala	Thr	Gly	Phe	Leu	Glu	
				770					775					780	
Tyr	Phe	Asp	Leu	Asn	Thr	Asp	Pro	Tyr	Gln	Leu	Met	Asn	Ala	Val	
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Asn	Thr	Leu	Asp	Arg	Asp	Val	Leu	Asn	Gln	Leu	His	Val	Gln	Leu	
				800					805					810	
Met	Glu	Leu	Arg	Ser	Cys	Lys	Gly	Tyr	Lys	Gln	Cys	Asn	Pro	Arg	
				815					820					825	
Thr	Arg	Asn	Met	Asp	Leu	Asp	Gly	Gly	Ser	Tyr	Glu	Gln	Tyr	Arg	
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Gln	Phe	Gln	Arg	Arg	Lys	Trp	Pro	Glu	Met	Lys	Arg	Pro	Ser	Ser	
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<213> Artificial Sequence

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 <210> 86
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 <210> 87
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<210> 91
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<213> Artificial Sequence

<220>
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<210> 92
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<400> 92
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<210> 93
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<210> 94
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 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 97
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 35 40 45
 Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr
 50 55 60
 Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg
 65 70 75

Ser	Ile	Ala	Val	Tyr	Tyr	Asp	Asn	Pro	His	Met	Val	Pro	Pro	Asp	
				80					85					90	
Lys	Cys	Arg	Cys	Ala	Val	Gly	Ser	Ile	Leu	Ser	Glu	Gly	Glu	Glu	
				95					100					105	
Ser	Pro	Ser	Pro	Glu	Leu	Ile	Asp	Leu	Tyr	Gln	Lys	Phe	Gly	Phe	
				110					115					120	
Lys	Val	Phe	Ser	Phe	Pro	Ala	Pro	Ser	His	Val	Val	Thr	Ala	Thr	
				125					130					135	
Phe	Pro	Tyr	Thr	Thr	Ile	Leu	Ser	Ile	Trp	Leu	Ala	Thr	Arg	Arg	
				140					145					150	
Val	His	Pro	Ala	Leu	Asp	Thr	Tyr	Ile	Lys	Glu	Arg	Lys	Leu	Cys	
				155					160					165	
Ala	Tyr	Pro	Arg	Leu	Glu	Ile	Tyr	Gln	Glu	Asp	Gln	Ile	His	Phe	
				170					175					180	
Met	Cys	Pro	Leu	Ala	Arg	Gln	Gly	Asp	Phe	Tyr	Val	Pro	Glu	Met	
				185					190					195	
Lys	Glu	Thr	Glu	Trp	Lys	Trp	Arg	Gly	Leu	Val	Glu	Ala	Ile	Asp	
				200					205					210	
Thr	Gln	Val	Asp	Gly	Thr	Gly	Ala	Asp	Thr	Met	Ser	Asp	Thr	Ser	
				215					220					225	
Ser	Val	Ser	Leu	Glu	Val	Ser	Pro	Gly	Ser	Arg	Glu	Thr	Ser	Ala	
				230					235					240	
Ala	Thr	Leu	Ser	Pro	Gly	Ala	Ser	Ser	Arg	Gly	Trp	Asp	Asp	Gly	
				245					250					255	
Asp	Thr	Arg	Ser	Glu	His	Ser	Tyr	Ser	Glu	Ser	Gly	Ala	Ser	Gly	
				260					265					270	
Ser	Ser	Phe	Glu	Glu	Leu	Asp	Leu	Glu	Gly	Glu	Gly	Pro	Leu	Gly	
				275					280					285	
Glu	Ser	Arg	Leu	Asp	Pro	Gly	Thr	Glu	Pro	Leu	Gly	Thr	Thr	Lys	
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Trp	Leu	Trp	Glu	Pro	Thr	Ala	Pro	Glu	Lys	Gly	Lys	Glu			
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<210> 98

<211> 725

<212> DNA

<213> Homo sapiens

<400> 98

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ctgaggctgg gctcgaaacc gaaagtcccg tccggaccct ccaagtggag 200

accctggtgg agccccaga accatgtgcc gagcccgtg cttttggaga 250

Demographic Data		Sociodemographic Data		Clinical Data		Treatment Data		Outcome Data	
Variable	Mean (SD)	Variable	Mean (SD)	Variable	Mean (SD)	Variable	Mean (SD)	Variable	Mean (SD)
Age	35.2 (12.5)	Gender	50% Male	Duration of illness	12.3 (8.7)	Number of hospitalizations	3.2 (2.1)	Number of relapses	2.1 (1.5)
Education	12.1 (2.3)	Marital status	45% Married	Previous treatment	78% Yes	Current treatment	85% Yes	Number of visits	15.4 (10.2)
Income	\$15,000 (10,000)	Employment	30% Employed	Family size	3.1 (1.2)	Family support	65% High	Number of medications	4.5 (3.2)
Religion	60% Christian	Health insurance	55% Private	Comorbidities	25% Yes	Adherence	70% High	Number of side effects	1.2 (0.8)
Living situation	50% Alone	Access to care	60% Easy	Stress level	4.2 (2.1)	Quality of life	5.1 (2.3)	Number of hospitalizations	3.2 (2.1)
Substance use	10% Yes	Smoking status	35% Smoker	Alcohol consumption	20% Yes	Physical activity	30% Yes	Number of visits	15.4 (10.2)
Family history	15% Yes	Genetic testing	10% Yes	Previous surgery	5% Yes	Current surgery	10% Yes	Number of medications	4.5 (3.2)
Comorbidities	25% Yes	Chronic conditions	15% Yes	Acute conditions	10% Yes	Stress management	40% High	Number of side effects	1.2 (0.8)
Medication adherence	70% High	Health literacy	60% High	Health beliefs	55% High	Health expectations	65% High	Number of hospitalizations	3.2 (2.1)
Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of visits	15.4 (10.2)
Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Number of medications	4.5 (3.2)
Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of side effects	1.2 (0.8)
Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Number of hospitalizations	3.2 (2.1)
Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of visits	15.4 (10.2)
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Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of side effects	1.2 (0.8)
Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Number of hospitalizations	3.2 (2.1)
Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of visits	15.4 (10.2)
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Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of side effects	1.2 (0.8)
Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Number of hospitalizations	3.2 (2.1)
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Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of visits	15.4 (10.2)
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Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Number of hospitalizations	3.2 (2.1)
Health beliefs	55% High	Health expectations	65% High	Health beliefs	55% High	Health expectations	65% High	Number of visits	15.4 (10.2)

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Demographics		Clinical		Laboratory		Immunology		Pathology		Genetics		Treatment		Outcome							
Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value						
Age (years)	55.2	Sex (male/female)	12/8	Weight (kg)	78.5	Height (cm)	175.3	BMI (kg/m ²)	25.8	SBP (mmHg)	145.2	DBP (mmHg)	95.1	HR (b/min)	72.5	ECG (normal/abnormal)	10/10				
Smoking (yes/no)	8/12	Alcohol (yes/no)	5/13	Diabetes (yes/no)	3/13	Hypertension (yes/no)	10/3	Cholesterol (mmol/L)	5.2	Triglycerides (mmol/L)	1.8	Glucose (mmol/L)	5.5	Urea (mmol/L)	4.2	Creatinine (mmol/L)	0.8	ESR (mm/h)	25.1		
Family history (yes/no)	5/10	Previous MI (yes/no)	2/11	Previous stroke (yes/no)	1/12	Previous PVD (yes/no)	3/10	Autoantibodies (yes/no)	4/9	ANCA (yes/no)	3/10	Anti-CCP (yes/no)	2/11	Anti-dsDNA (yes/no)	1/12	Anti-Smith (yes/no)	0/13	Anti-Ro (yes/no)	1/13		
Medications (yes/no)	10/3	Aspirin (yes/no)	8/5	Statins (yes/no)	7/6	Beta-blockers (yes/no)	6/7	ACE inhibitors (yes/no)	5/8	Diuretics (yes/no)	4/9	Anticoagulants (yes/no)	3/10	Immunosuppressants (yes/no)	2/11	Antibiotics (yes/no)	1/12	Antidepressants (yes/no)	0/13		
Comorbidities (yes/no)	9/4	Chronic kidney disease (yes/no)	2/11	Chronic liver disease (yes/no)	1/12	Chronic lung disease (yes/no)	3/10	Chronic heart failure (yes/no)	4/9	Chronic pain (yes/no)	5/8	Chronic fatigue (yes/no)	6/7	Chronic anxiety (yes/no)	3/10	Chronic depression (yes/no)	2/11	Chronic insomnia (yes/no)	1/12	Chronic constipation (yes/no)	0/13
Family size (yes/no)	7/6	Family income (yes/no)	8/5	Family education (yes/no)	9/4	Family occupation (yes/no)	10/3	Family social support (yes/no)	11/2	Family health status (yes/no)	12/1	Family lifestyle (yes/no)	13/0	Family environment (yes/no)	14/0	Family culture (yes/no)	15/0	Family religion (yes/no)	16/0		
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<210> 113
 <211> 610
 <212> PRT
 <213> Homo sapiens

<400> 113
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 35 40 45
 Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser
 50 55 60
 Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser
 65 70 75
 Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly
 80 85 90
 Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys
 95 100 105

Cys	His	Thr	Phe	Gly	Lys	Asn	Gly	Leu	Glu	Phe	Asp	Thr	Gly	Ile	110	115	120
His	Tyr	Ile	Gly	Arg	Met	Glu	Glu	Gly	Ser	Ile	Gly	Arg	Phe	Ile	125	130	135
Leu	Asp	Gln	Ile	Thr	Glu	Gly	Gln	Leu	Asp	Trp	Ala	Pro	Leu	Ser	140	145	150
Ser	Pro	Phe	Asp	Ile	Met	Val	Leu	Glu	Gly	Pro	Asn	Gly	Arg	Lys	155	160	165
Glu	Tyr	Pro	Met	Tyr	Ser	Gly	Glu	Lys	Ala	Tyr	Ile	Gln	Gly	Leu	170	175	180
Lys	Glu	Lys	Phe	Pro	Gln	Glu	Glu	Ala	Ile	Ile	Asp	Lys	Tyr	Ile	185	190	195
Lys	Leu	Val	Lys	Val	Val	Ser	Ser	Gly	Ala	Pro	His	Ala	Ile	Leu	200	205	210
Leu	Lys	Phe	Leu	Pro	Leu	Pro	Val	Val	Gln	Leu	Leu	Asp	Arg	Cys	215	220	225
Gly	Leu	Leu	Thr	Arg	Phe	Ser	Pro	Phe	Leu	Gln	Ala	Ser	Thr	Gln	230	235	240
Ser	Leu	Ala	Glu	Val	Leu	Gln	Gln	Leu	Gly	Ala	Ser	Ser	Glu	Leu	245	250	255
Gln	Ala	Val	Leu	Ser	Tyr	Ile	Phe	Pro	Thr	Tyr	Gly	Val	Thr	Pro	260	265	270
Asn	His	Ser	Ala	Phe	Ser	Met	His	Ala	Leu	Leu	Val	Asn	His	Tyr	275	280	285
Met	Lys	Gly	Gly	Phe	Tyr	Pro	Arg	Gly	Gly	Ser	Ser	Glu	Ile	Ala	290	295	300
Phe	His	Thr	Ile	Pro	Val	Ile	Gln	Arg	Ala	Gly	Gly	Ala	Val	Leu	305	310	315
Thr	Lys	Ala	Thr	Val	Gln	Ser	Val	Leu	Leu	Asp	Ser	Ala	Gly	Lys	320	325	330
Ala	Cys	Gly	Val	Ser	Val	Lys	Lys	Gly	His	Glu	Leu	Val	Asn	Ile	335	340	345
Tyr	Cys	Pro	Ile	Val	Val	Ser	Asn	Ala	Gly	Leu	Phe	Asn	Thr	Tyr	350	355	360
Glu	His	Leu	Leu	Pro	Gly	Asn	Ala	Arg	Cys	Leu	Pro	Gly	Val	Lys	365	370	375
Gln	Gln	Leu	Gly	Thr	Val	Arg	Pro	Gly	Leu	Gly	Met	Thr	Ser	Val	380	385	390
Phe	Ile	Cys	Leu	Arg	Gly	Thr	Lys	Glu	Asp	Leu	His	Leu	Pro	Ser	395	400	405
Thr	Asn	Tyr	Tyr	Val	Tyr	Tyr	Asp	Thr	Asp	Met	Asp	Gln	Ala	Met	410	415	420

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<210> 115

<211> 301

<212> PRT

<213> Homo sapiens

<400> 115

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Leu	Ser	Leu	Ala	Ser	Ala	Ser	Ser	Asp	Glu	Glu	Gly	Ser	Gln	Asp
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Glu	Ser	Leu	Asp	Ser	Lys	Thr	Thr	Leu	Thr	Ser	Asp	Glu	Ser	Val
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Lys	Asp	His	Thr	Thr	Ala	Gly	Arg	Val	Val	Ala	Gly	Gln	Ile	Phe
				50					55					60
Leu	Asp	Ser	Glu	Glu	Ser	Glu	Leu	Glu	Ser	Ser	Ile	Gln	Glu	Glu
				65					70					75
Glu	Asp	Ser	Leu	Lys	Ser	Gln	Glu	Gly	Glu	Ser	Val	Thr	Glu	Asp
				80					85					90
Ile	Ser	Phe	Leu	Glu	Ser	Pro	Asn	Pro	Glu	Asn	Lys	Asp	Tyr	Glu
				95					100					105
Glu	Pro	Lys	Lys	Val	Arg	Lys	Pro	Ala	Leu	Thr	Ala	Ile	Glu	Gly
				110					115					120
Thr	Ala	His	Gly	Glu	Pro	Cys	His	Phe	Pro	Phe	Leu	Phe	Leu	Asp
				125					130					135
Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp	Gly	Arg	Glu	Asp	Gly	Arg
				140					145					150
Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys	Ala	Asp	Glu	Lys	Trp
				155					160					165
Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met
				170					175					180
Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys	Ile	Leu	Asn
				185					190					195
Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg	Tyr	Leu
				200					205					210
Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg	Val
				215					220					225
Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln
				230					235					240
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro
				245					250					255
Lys	Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly
				260					265					270
Val	Asn	Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly
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Ala	Leu	Gly	Gly	Asn	Leu	Ile	Ala	His	Met	Val	Leu	Val	Ser	Arg
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<210> 116
 <211> 584
 <212> DNA
 <213> Homo sapiens

<400> 116

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<210> 117
 <211> 123
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 His Val Thr Ile Arg Asp Tyr Gly Val Ser Trp Tyr Gln Gln Arg
 50 55 60
 Ala Gly Ser Ala Pro Arg Tyr Leu Leu Tyr Tyr Arg Ser Glu Glu
 65 70 75
 Asp His His Arg Pro Ala Asp Ile Pro Asp Arg Phe Ser Ala Ala
 80 85 90
 Lys Asp Glu Ala His Asn Ala Cys Val Leu Thr Ile Ser Pro Val
 95 100 105
 Gln Pro Glu Asp Asp Ala Asp Tyr Tyr Cys Ser Val Gly Tyr Gly
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 Phe Ser Pro

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 <211> 3402
 <212> DNA
 <213> Homo sapiens

<400> 118

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Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
				260					265					270
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
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Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly
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Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
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Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
				320					325					330
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
				335					340					345
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys
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Pro	Pro	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu
				365					370					375
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile
				380					385					390
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro
				395					400					405
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro
				410					415					420
Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu
				425					430					435
Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His
				440					445					450
Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
				455					460					465
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr
				470					475					480
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

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<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

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<210> 122

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

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<210> 123

<211> 4420

<212> DNA

<213> Homo sapiens

<400> 123

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 cagcgagcga gcaggggtg ccagcgccag ggtggagtgg tggcctctct 3650
 gagatttcct agagttgctc aacagcccct gatcaactaa gttttgtggt 3700
 acttcaccct cttctgccct catttcatgt gacagccatt gtgagactga 3750
 tgcacaaact gtcacttggg taattttaagc acttctgttt tcgtgaattt 3800
 gcttgtttgt ttcttcatgc ctttacttac tttgtcccat gctactgatt 3850
 ggcacgtggc cccacaatg gcacaataaa gccctttgt gaaactgttc 3900
 tttaaatgaa acacaagaaa ttggccactg gtaaaactct gcagcttcaa 3950
 ctgtacttca tttaatgcca ttaatgaaa tatacttctt cttctttttg 4000
 catgggtttg cccacctctg caatagtgat aatctgatgc tgaagatcaa 4050

ataaccaata taaagcatat ttcttggcct tgctccacag gacataggca 4100
 agccttgatc atagttcata catataaatg gtggtgaaat aaagaaataa 4150
 aacacaatac ttttacttga aatgtaaata acttatttat ttctttgcta 4200
 aatttgggaat tctagtgcac attcaaagt tt aagctattaa atatagggtg 4250
 atcatagttc ctctaccaag tctggaaaga acatctcctg gtatccacaa 4300
 ttacaccagg ttgctaactg tatttgtaca tttccctttg cattcgcttt 4350
 tgttcttgct agaaaccag ttagtagccag ggcagatgtc aataaatgca 4400
 tactctgtat ttcgaaaaaa 4420

<210> 124
 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 124
 Met Val Gly Thr Lys Ala Trp Val Phe Ser Phe Leu Val Leu Glu
 1 5 10 15
 Val Thr Ser Val Leu Gly Arg Gln Thr Met Leu Thr Gln Ser Val
 20 25 30
 Arg Arg Val Gln Pro Gly Lys Lys Asn Pro Ser Ile Phe Ala Lys
 35 40 45
 Pro Ala Asp Thr Leu Glu Ser Pro Gly Glu Trp Thr Thr Trp Phe
 50 55 60
 Asn Ile Asp Tyr Pro Gly Gly Lys Gly Asp Tyr Glu Arg Leu Asp
 65 70 75
 Ala Ile Arg Phe Tyr Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu
 80 85 90
 Arg Leu Glu Ala Arg Thr Thr Asp Trp Thr Pro Ala Gly Ser Thr
 95 100 105
 Gly Gln Val Val His Gly Ser Pro Arg Glu Gly Phe Trp Cys Leu
 110 115 120
 Asn Arg Glu Gln Arg Pro Gly Gln Asn Cys Ser Asn Tyr Thr Val
 125 130 135
 Arg Phe Leu Cys Pro Pro Gly Ser Leu Arg Arg Asp Thr Glu Arg
 140 145 150
 Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys Cys Ser Ala Ala Cys
 155 160 165
 Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile Cys Leu Ala Glu
 170 175 180
 Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly Gln His Cys
 185 190 195
 Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro Met Gly
 200 205 210

Phe Thr Leu His Val Pro Gln Asp Thr Glu Arg Leu Val Leu Thr	530	535	540
Phe Val Asp Arg Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu	545	550	555
Pro Phe Asn Lys Lys Gly Ser Ala Val Phe His Glu Ile Lys Met	560	565	570
Leu Arg Arg Lys Glu Pro Ile Thr Leu Glu Ala Met Glu Thr Asn	575	580	585
Ile Ile Pro Leu Gly Glu Val Val Gly Glu Asp Pro Met Ala Glu	590	595	600
Leu Glu Ile Pro Ser Arg Ser Phe Tyr Arg Gln Asn Gly Glu Pro	605	610	615
Tyr Ile Gly Lys Val Lys Ala Ser Val Thr Phe Leu Asp Pro Arg	620	625	630
Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr Asp Leu Asn Phe Ile	635	640	645
Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr Tyr Gly Met Phe	650	655	660
Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro Leu Asn Ala	665	670	675
Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys Met Pro	680	685	690
Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp Thr	695	700	705
Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg	710	715	720
Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu	725	730	735
Ile Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg	740	745	750
Arg Cys Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu	755	760	765
Pro Ser Glu Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu	770	775	780
Glu Pro Arg Thr Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg	785	790	795
Phe Asp Ser Val Ile Thr Gly Pro Asn Gly Ala Cys Val Pro Ala	800	805	810
Phe Cys Asp Asp Gln Ser Pro Asp Ala Tyr Ser Ala Tyr Val Leu	815	820	825
Ala Ser Leu Ala Gly Glu Glu Leu Gln Ala Val Glu Ser Ser Pro	830	835	840

Lys Phe Asn Pro	Asn Ala Ile Gly Val	Pro Gln Pro Tyr Leu Asn	845	850	855
Lys Leu Asn Tyr	Arg Arg Thr Asp His	Glu Asp Pro Arg Val Lys	860	865	870
Lys Thr Ala Phe	Gln Ile Ser Met Ala	Lys Pro Arg Pro Asn Ser	875	880	885
Ala Glu Glu Ser	Asn Gly Pro Ile Tyr	Ala Phe Glu Asn Leu Arg	890	895	900
Ala Cys Glu Glu	Ala Pro Pro Ser Ala	Ala His Phe Arg Phe Tyr	905	910	915
Gln Ile Glu Gly	Asp Arg Tyr Asp Tyr	Asn Thr Val Pro Phe Asn	920	925	930
Glu Asp Asp Pro	Met Ser Trp Thr Glu	Asp Tyr Leu Ala Trp Trp	935	940	945
Pro Lys Pro Met	Glu Phe Arg Ala Cys	Tyr Ile Lys Val Lys Ile	950	955	960
Val Gly Pro Leu	Glu Val Asn Val Arg	Ser Arg Asn Met Gly Gly	965	970	975
Thr His Arg Arg	Thr Val Gly Lys Leu	Tyr Gly Ile Arg Asp Val	980	985	990
Arg Ser Thr Arg	Asp Arg Asp Gln Pro	Asn Val Ser Ala Ala Cys	995	1000	1005
Leu Glu Phe Lys	Cys Ser Gly Met Leu	Tyr Asp Gln Asp Arg Val	1010	1015	1020
Asp Arg Thr Leu	Val Lys Val Ile Pro	Gln Gly Ser Cys Arg Arg	1025	1030	1035
Ala Ser Val Asn	Pro Met Leu His Glu	Tyr Leu Val Asn His Leu	1040	1045	1050
Pro Leu Ala Val	Asn Asn Asp Thr Ser	Glu Tyr Thr Met Leu Ala	1055	1060	1065
Pro Leu Asp Pro	Leu Gly His Asn Tyr	Gly Ile Tyr Thr Val Thr	1070	1075	1080
Asp Gln Asp Pro	Arg Thr Ala Lys Glu	Ile Ala Leu Gly Arg Cys	1085	1090	1095
Phe Asp Gly Thr	Ser Asp Gly Ser Ser	Arg Ile Met Lys Ser Asn	1100	1105	1110
Val Gly Val Ala	Leu Thr Phe Asn Cys	Val Glu Arg Gln Val Gly	1115	1120	1125
Arg Gln Ser Ala	Phe Gln Tyr Leu Gln	Ser Thr Pro Ala Gln Ser	1130	1135	1140
Pro Ala Ala Gly	Thr Val Gln Gly Arg	Val Pro Ser Arg Arg Gln	1145	1150	1155

Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala
1160 1165 1170

Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn
1175 1180

<210> 125
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 125
ctggtgcctc aacagggagc ag 22

<210> 126
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 126
ccattgtgca ggtcagggtca cag 23

<210> 127
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 127
ctggagcaag tgctcagctg cctgtgggtca gactgggggtc 40

<210> 128
<211> 2819
<212> DNA
<213> Homo sapiens

<400> 128
ctgcaagttg ttaacgccta acacacaagt atgttaggct tccaccaaag 50
tcctcaatat acctgaatac gcacaatatc ttaactcttc atatttggtt 100
ttgggatctg ctttgagggtc ccatcttcat ttaaaaaaaa atacagagac 150
ctacctaccc gtacgcatac atacatatgt gtatatatat gtaaaactaga 200
caaagatcgc agatcataaa gcaagctctg ctttagtttc caagaagatt 250
acaaagaatt tagagatgta tttgtcaaga tccctgtcga ttcatgccct 300
ttgggttacg gtgtcctcag tgatgcagcc ctaccctttg gtttggggac 350
attatgattt gtgtaagact cagatttaca cggaagaagg gaaagtttgg 400
gattacatgg cctgccagcc ggaatccacg gacatgacaa aatatctgaa 450

	125		130		135
Leu Ser Trp Ser	Lys Thr Ile Glu Leu	Thr Asp Asn Ile Val	Ile		
	140		145		150
Thr Phe Glu Ser	Gly Arg Pro Asp Gln	Met Ile Leu Glu Lys	Ser		
	155		160		165
Leu Asp Tyr Gly	Arg Thr Trp Gln Pro	Tyr Gln Tyr Tyr Ala	Thr		
	170		175		180
Asp Cys Leu Asp	Ala Phe His Met Asp	Pro Lys Ser Val Lys	Asp		
	185		190		195
Leu Ser Gln His	Thr Val Leu Glu Ile	Ile Cys Thr Glu Glu	Tyr		
	200		205		210
Ser Thr Gly Tyr	Thr Thr Asn Ser Lys	Ile Ile His Phe Glu	Ile		
	215		220		225
Lys Asp Arg Phe	Ala Leu Phe Ala Gly	Pro Arg Leu Arg Asn	Met		
	230		235		240
Ala Ser Leu Tyr	Gly Gln Leu Asp Thr	Thr Lys Lys Leu Arg	Asp		
	245		250		255
Phe Phe Thr Val	Thr Asp Leu Arg Ile	Arg Leu Leu Arg Pro	Ala		
	260		265		270
Val Gly Glu Ile	Phe Val Asp Glu Leu	His Leu Ala Arg Tyr	Phe		
	275		280		285
Tyr Ala Ile Ser	Asp Ile Lys Val Arg	Gly Arg Cys Lys Cys	Asn		
	290		295		300
Leu His Ala Thr	Val Cys Val Tyr Asp	Asn Ser Lys Leu Thr	Cys		
	305		310		315
Glu Cys Glu His	Asn Thr Thr Gly Pro	Asp Cys Gly Lys Cys	Lys		
	320		325		330
Lys Asn Tyr Gln	Gly Arg Pro Trp Ser	Pro Gly Ser Tyr Leu	Pro		
	335		340		345
Ile Pro Lys Gly	Thr Ala Asn Thr Cys	Ile Pro Ser Ile Ser	Ser		
	350		355		360
Ile Gly Thr Asn	Val Cys Asp Asn Glu	Leu Leu His Cys Gln	Asn		
	365		370		375
Gly Gly Thr Cys	His Asn Asn Val Arg	Cys Leu Cys Pro Ala	Ala		
	380		385		390
Tyr Thr Gly Ile	Leu Cys Glu Lys Leu	Arg Cys Glu Glu Ala	Gly		
	395		400		405
Ser Cys Gly Ser	Asp Ser Gly Gln Gly	Ala Pro Pro His Gly	Thr		
	410		415		420
Pro Ala Leu Leu	Leu Leu Thr Thr Leu	Leu Gly Thr Ala Ser	Pro		
	425		430		435
Leu Val Phe					

<210> 130
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 130
tcgattatgg acgaacatgg cagc 24

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 131
ttctgagatc cctcatcctc 20

<210> 132
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 132
aggttcaggg acagcaagtt tggg 24

<210> 133
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
tttgctggac ctcggtacg gaattggctt ccctctacgg acagctggat 50

<210> 134
<211> 1493
<212> DNA
<213> Homo sapiens

<400> 134
cccacgcgtc cgggtgacct gggccgagcc ctcccggtcg gctaagattg 50
ctgaggaggc ggcgggtagc tggcaggcgc cgacttcoga aggcgcgcgt 100
ccgggcgagg tgtcctcatg acttctcttg tggaccatgt ccgtgatott 150
ttttgcctgc gtggtacggg taagggatgg actgcccctc tcagcctcta 200
ctgattttta ccacacccaa gatttttttg aatggaggag acggctcaag 250
agtttagcct tgcgactggc ccagtatcca ggctcgagggt ctgcagaagg 300

ttgtgacttt agtatacatt tttcttcttt cggggacgtg gcctgcatgg 350
 ctatctgctc ctgccagtgt ccagcagcca tggccttctg cttcctggag 400
 accctgtggt gggaattcac agcttctat gacactacct gcattggcct 450
 agcctccagg ccatacgtt ttcttgagtt tgacagcatc attcagaaag 500
 tgaagtggca ttttaactat gtaagttcct ctcagatgga gtgcagcttg 550
 gaaaaaattc aggaggagct caagttgcag cctccagcgg ttctcactct 600
 ggaggacaca gatgtggcaa atggggtgat gaatggtcac acaccgatgc 650
 acttgagacc tgctcctaatt ttccgaatgg aaccagtgc agccctgggt 700
 atcctctccc tcattctcaa catcatgtgt gctgccctga atctcattcg 750
 aggagttcac cttgcagaac attctttaca ggatccaagg agctggttct 800
 gctggttga ccaaacctcg tgagccagcc acccctgacc caaatgagga 850
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 gggaaatctc atcagcaggg agcctgtgga aaagggcatg tcagtgaat 950
 ctgggaatgg ctggattcgg aaacatctgc ccatgtgtat tgatggcaga 1000
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 atatgattct ggggttgctt cagaagtgtt atttcatgaa tcattcatat 1150
 gatttgatcc ccaggattc tattttgttt aatgggcttt tctactaaaa 1200
 gcataaaata ctgaggctga tttagtcagg gcaaaaccat ttactttaca 1250
 tattcgtttt caatacttgc tgttcatgtt acacaagctt cttacggttt 1300
 tcttgtaaca ataaatattt tgagtaaata atgggtacat ttttaacaaac 1350
 tcagtagtac aacctaaact tgtataaaag tgtgtaaaaa tgtatagcca 1400
 tttatatcct atgtataaat taaatgaggt ggcttcagaa atggcagaat 1450
 aaatctaaag tgtttattaa aaaaaaaaaa aaaaaaaaaa aag 1493

<210> 135

<211> 228

<212> PRT

<213> Homo sapiens

<400> 135

Met	Ser	Val	Ile	Phe	Phe	Ala	Cys	Val	Val	Arg	Val	Arg	Asp	Gly
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Leu	Pro	Leu	Ser	Ala	Ser	Thr	Asp	Phe	Tyr	His	Thr	Gln	Asp	Phe
				20					25					30
Leu	Glu	Trp	Arg	Arg	Arg	Leu	Lys	Ser	Leu	Ala	Leu	Arg	Leu	Ala
				35					40					45

Gln	Tyr	Pro	Gly	Arg	Gly	Ser	Ala	Glu	Gly	Cys	Asp	Phe	Ser	Ile	
				50					55					60	
His	Phe	Ser	Ser	Phe	Gly	Asp	Val	Ala	Cys	Met	Ala	Ile	Cys	Ser	
				65					70					75	
Cys	Gln	Cys	Pro	Ala	Ala	Met	Ala	Phe	Cys	Phe	Leu	Glu	Thr	Leu	
				80					85					90	
Trp	Trp	Glu	Phe	Thr	Ala	Ser	Tyr	Asp	Thr	Thr	Cys	Ile	Gly	Leu	
				95					100					105	
Ala	Ser	Arg	Pro	Tyr	Ala	Phe	Leu	Glu	Phe	Asp	Ser	Ile	Ile	Gln	
				110					115					120	
Lys	Val	Lys	Trp	His	Phe	Asn	Tyr	Val	Ser	Ser	Ser	Gln	Met	Glu	
				125					130					135	
Cys	Ser	Leu	Glu	Lys	Ile	Gln	Glu	Glu	Leu	Lys	Leu	Gln	Pro	Pro	
				140					145					150	
Ala	Val	Leu	Thr	Leu	Glu	Asp	Thr	Asp	Val	Ala	Asn	Gly	Val	Met	
				155					160					165	
Asn	Gly	His	Thr	Pro	Met	His	Leu	Glu	Pro	Ala	Pro	Asn	Phe	Arg	
				170					175					180	
Met	Glu	Pro	Val	Thr	Ala	Leu	Gly	Ile	Leu	Ser	Leu	Ile	Leu	Asn	
				185					190					195	
Ile	Met	Cys	Ala	Ala	Leu	Asn	Leu	Ile	Arg	Gly	Val	His	Leu	Ala	
				200					205					210	
Glu	His	Ser	Leu	Gln	Asp	Pro	Arg	Ser	Trp	Phe	Cys	Trp	Leu	Asp	
				215					220					225	

Gln Thr Ser

<210> 136
 <211> 239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 61, 143, 209
 <223> unknown base

<400> 136
 tgcttcctgg agaccctgtg gtgggaattc acagcttont atgacactac 50
 ctgcattggc ntagcctcca ggccatacgc ttttcttgag tttgacagca 100
 tcattcagaa agtgaagtgg cattttaact atgtaagttc ctntcagatg 150
 gagtgcagct tggaaaaaat tcaggaggag ctcaagttgc agcctccagc 200
 ggttctcant atggaggaca cagatgtggc aaatggggt 239

<210> 137
 <211> 2300
 <212> DNA

[illegible]

400> 137

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acgtgagcgc	gacccgacct	taaagagtgg	ggagcaaagg	gaggacagag	100
ccctttaaaa	cgaggcggggt	ggtgcctgcc	cctttaagggt	cggggcggtcc	150
ggacgactgt	atctgagccc	cagactgccc	cgagtttctg	tgcagggtcg	200
cgaggaaaagg	cccctagggt	gggtctgggt	gcttggcggc	ggcggttcc	250
tccccgctcg	tcctccccgg	gccagaggc	acctcggtt	cagtcatgct	300
gagcagagta	tggaagcacc	tgactacgaa	gtgctatccg	tgcgagaaca	350
gctattccac	gagaggatcc	gcgagtgtat	tatatcaaca	cttctgtttg	400
caacactgta	catcctctgc	cacatcttcc	tgaccgctt	caagaagcct	450
gctgagttca	ccacagtgga	tgatgaagat	gccaccgtca	acaagattgc	500
gctcgagctg	tgcaccttta	cctggcaat	tgccctgggt	gctgtcctgc	550
tcctgccctt	ctccatcatc	agcaatgagg	tgctgctctc	cctgcctcgg	600
aactactaca	tccagtggct	caacggctcc	ctcatccatg	gcctctggaa	650
ccttggtttt	ctcttcccc	acctgtccct	catcttcctc	atgccctttg	700
catatttctt	cactgagtct	gagggctttg	ctggctccag	aaaggggtgc	750
ctggggccggg	tctatgagac	agtggtgatg	ttgatgtctc	tcactctgct	800
ggtgctaggt	atggtgtggg	tggcatcagc	cattgtggac	aagaacaagg	850
ccaacagaga	gtcactctat	gacttttggg	agtactatct	cccctacctc	900
tactcatgca	tctccttcc	tggggttctg	ctgctcctgg	tgtgtactcc	950
actgggtctc	gcccgcattg	tctccgtcac	tgggaagctg	ctagtcaagc	1000
cccggctgct	ggaagacctg	gaggagcagc	tgtactgctc	agcctttgag	1050
gaggcagccc	tgaccgcgag	gatctgtaat	cctacttcc	gctggctgcc	1100
tttagacatg	gagctgctac	acagacaggt	cctggctctg	cagacacaga	1150
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gctcattgtg	gccatccaca	tcctggagct	gctcatcgat	gaggctgcc	1300
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ggccagatg	gcacgacact	gccatgacgc	agataattgg	gaactgtgtc	1500

tgtctcctgg tctaagctc agcacttcct gtcttctctc gaaccctggg 1550
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 gcaatttcta cattgtgttc ctctacaacg cagcctttgc aggcctcacc 1650
 acactctgtc tgggtgaagac cttcactgca gctgtgcggg cagagctgat 1700
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 tcgggagata gattgtotcc cttgcctctg gcccagcaga gcctaagcac 2200
 tgtgctatcc tggaggggct ttggaccacc tgaaagacca aggggatagg 2250
 gaggaggagg cttcagccat cagcaataaa gttgatccca gggaaaaaaaa 2300

<210> 138

<211> 489

<212> PRT

<213> Homo sapiens

<400> 138

Met	Glu	Ala	Pro	Asp	Tyr	Glu	Val	Leu	Ser	Val	Arg	Glu	Gln	Leu
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Phe	His	Glu	Arg	Ile	Arg	Glu	Cys	Ile	Ile	Ser	Thr	Leu	Leu	Phe
				20					25					30
Ala	Thr	Leu	Tyr	Ile	Leu	Cys	His	Ile	Phe	Leu	Thr	Arg	Phe	Lys
				35					40					45
Lys	Pro	Ala	Glu	Phe	Thr	Thr	Val	Asp	Asp	Glu	Asp	Ala	Thr	Val
				50					55					60
Asn	Lys	Ile	Ala	Leu	Glu	Leu	Cys	Thr	Phe	Thr	Leu	Ala	Ile	Ala
				65					70					75
Leu	Gly	Ala	Val	Leu	Leu	Leu	Pro	Phe	Ser	Ile	Ile	Ser	Asn	Glu
				80					85					90
Val	Leu	Leu	Ser	Leu	Pro	Arg	Asn	Tyr	Tyr	Ile	Gln	Trp	Leu	Asn
				95					100					105
Gly	Ser	Leu	Ile	His	Gly	Leu	Trp	Asn	Leu	Val	Phe	Leu	Phe	Pro
				110					115					120
Asn	Leu	Ser	Leu	Ile	Phe	Leu	Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr

	125	130	135
Glu Ser Glu Gly	Phe Ala Gly Ser Arg	Lys Gly Val Leu Gly	Arg
	140	145	150
Val Tyr Glu Thr	Val Val Met Leu Met	Leu Leu Thr Leu Leu	Val
	155	160	165
Leu Gly Met Val	Trp Val Ala Ser Ala	Ile Val Asp Lys Asn	Lys
	170	175	180
Ala Asn Arg Glu	Ser Leu Tyr Asp Phe	Trp Glu Tyr Tyr Leu	Pro
	185	190	195
Tyr Leu Tyr Ser	Cys Ile Ser Phe Leu	Gly Val Leu Leu Leu	Leu
	200	205	210
Val Cys Thr Pro	Leu Gly Leu Ala Arg	Met Phe Ser Val Thr	Gly
	215	220	225
Lys Leu Leu Val	Lys Pro Arg Leu Leu	Glu Asp Leu Glu Glu	Gln
	230	235	240
Leu Tyr Cys Ser	Ala Phe Glu Glu Ala	Ala Leu Thr Arg Arg	Ile
	245	250	255
Cys Asn Pro Thr	Ser Cys Trp Leu Pro	Leu Asp Met Glu Leu	Leu
	260	265	270
His Arg Gln Val	Leu Ala Leu Gln Thr	Gln Arg Val Leu Leu	Glu
	275	280	285
Lys Arg Arg Lys	Ala Ser Ala Trp Gln	Arg Asn Leu Gly Tyr	Pro
	290	295	300
Leu Ala Met Leu	Cys Leu Leu Val Leu	Thr Gly Leu Ser Val	Leu
	305	310	315
Ile Val Ala Ile	His Ile Leu Glu Leu	Leu Ile Asp Glu Ala	Ala
	320	325	330
Met Pro Arg Gly	Met Gln Gly Thr Ser	Leu Gly Gln Val Ser	Phe
	335	340	345
Ser Lys Leu Gly	Ser Phe Gly Ala Val	Ile Gln Val Val Leu	Ile
	350	355	360
Phe Tyr Leu Met	Val Ser Ser Val Val	Gly Phe Tyr Ser Ser	Pro
	365	370	375
Leu Phe Arg Ser	Leu Arg Pro Arg Trp	His Asp Thr Ala Met	Thr
	380	385	390
Gln Ile Ile Gly	Asn Cys Val Cys Leu	Leu Val Leu Ser Ser	Ala
	395	400	405
Leu Pro Val Phe	Ser Arg Thr Leu Gly	Leu Thr Arg Phe Asp	Leu
	410	415	420
Leu Gly Asp Phe	Gly Arg Phe Asn Trp	Leu Gly Asn Phe Tyr	Ile
	425	430	435
Val Phe Leu Tyr	Asn Ala Ala Phe Ala	Gly Leu Thr Thr Leu	Cys

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<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

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<210> 142

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142

tcagcaatga ggtgctgctc 20

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

tgaggaagat gagggacagg ttgg 24

<210> 144

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 144

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<210> 145

<211> 685

<212> DNA

<213> Homo sapiens

<400> 145

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tgggtccaggt cttcatgctg ctgtgggtga tattactggt cctggctcct 150

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<211> 1621
<212> DNA
<213> Homo sapiens
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126

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<210> 148
 <211> 358
 <212> PRT

<213> Homo sapiens

<400> 148

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				20					25					30
Gly	Val	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr
				35					40					45
Arg	Lys	Leu	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp
				50					55					60
Pro	Gln	Ala	Gln	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu
				65					70					75
Val	Leu	Ser	Asp	Ser	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly
				80					85					90
Glu	Glu	Gly	Leu	Lys	Asp	Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile
				95					100					105
Phe	Ser	His	Phe	Phe	Gly	Asp	Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr
				110					115					120
Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile	Pro	Arg	Gly	Ser	Asp	Ile	Ile
				125					130					135
Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu	Val	Tyr	Ala	Gly	Asn	Phe
				140					145					150
Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala	Arg	Gln	Ala	Pro	Gly
				155					160					165
Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg	Thr	Thr	Gln	Leu
				170					175					180
Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp	Glu
				185					190					195
Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu	Val
				200					205					210
Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe	Ile
				215					220					225
Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
				230					235					240
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly
				245					250					255
Asp	Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser	Leu
				260					265					270
Val	Gly	Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys	Val
				275					280					285
His	Ile	Ser	Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Trp
				290					295					300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys
305 310 315

Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln
320 325 330

Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln
335 340 345

Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr
350 355

<210> 149
<211> 509
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,
482
<223> unknown base

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acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350
cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400
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<211> 1532
<212> DNA
<213> Homo sapiens

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gaccgggact gagtcaggag ccctctggaa gcatggagac tgtggtgatt 200
gttgccatag gtgtgctggc caccatcttt ctggttctgt ttgcagcctt 250
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<210> 151

<211> 226

<212> PRT

<213> Homo sapiens

<400> 151

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				20					25					30

Tyr	Cys	Arg	Pro	Arg	Asp	Leu	Leu	Gln	Arg	Tyr	Asp	Ser	Lys	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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<210> 153
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> N-myristoylation Sites
 <222> 11-16, 51-56 and 116-121
 <223> N-myristoylation Sites.

<220>
 <221> Transmembrane domains
 <222> 12-30, 33-52, 69-89 and 93-109
 <223> Transmembrane domains

<220>
 <221> Aminoacyl-transfer RNA Synthetases.
 <222> 49-59
 <223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153
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 Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly
 35 40 45
 Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe
 50 55 60

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<210> 156

<211> 378
 <212> PRT
 <213> Homo sapiens

<400> 156

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Val	Phe	Cys	Tyr	Val	Phe	Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	
				20					25					30	
Ile	Gln	Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	
				35					40					45	
Phe	Arg	Lys	Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	
				50					55					60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	
				65					70					75	
Phe	Thr	Asp	Pro	Arg	Ala	Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	
				80					85					90	
Ile	Val	Val	Leu	Asn	His	Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	
				95					100					105	
Trp	Ser	Leu	Ser	Glu	Arg	Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	
				110					115					120	
Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met	
				125					130					135	
Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln	
				140					145					150	
Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	
				155					160					165	
Pro	Glu	Lys	Tyr	Phe	Phe	Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Lys	Lys	His	Glu	Ile	Ser	Met	Gln	Val	Ala	Arg	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Arg	Leu	Lys	His	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Ala	Ile	Thr	Val	Arg	Ser	Leu	Arg	Asn	Val	Val	Ser	Ala	Val	
				215					220					225	
Tyr	Asp	Cys	Thr	Leu	Asn	Phe	Arg	Asn	Asn	Glu	Asn	Pro	Thr	Leu	
				230					235					240	
Leu	Gly	Val	Leu	Asn	Gly	Lys	Lys	Tyr	His	Ala	Asp	Leu	Tyr	Val	
				245					250					255	
Arg	Arg	Ile	Pro	Leu	Glu	Asp	Ile	Pro	Glu	Asp	Asp	Asp	Glu	Cys	
				260					265					270	
Ser	Ala	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Phe	Gln	
				275					280					285	
Glu	Glu	Tyr	Tyr	Arg	Thr	Gly	Thr	Phe	Pro	Glu	Thr	Pro	Met	Val	

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<210> 158
 <211> 409
 <212> PRT
 <213> Homo sapiens

<400> 158
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 35 40 45
 Thr Asp Ser Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp
 50 55 60
 Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn
 65 70 75
 Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser
 80 85 90
 Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg His
 95 100 105

Ser Asp Gln Ile	Met Thr Phe Arg Glu Arg	Leu Leu His Lys Asn
	110 115	120
Leu Gln Glu His	Phe Ser Asn Gln Asp Leu Val Phe Leu Leu	Leu
	125 130	135
Thr Pro Ser Ile	Ile Thr Glu Ser Cys Ser Thr His Arg Leu	Glu
	140 145	150
His Ser Leu Tyr	Lys Pro Gln Lys Gly Leu Phe His Arg Val	Pro
	155 160	165
Leu Val Val Ala	Asn Leu Gly Met Ser Glu Gln Leu Gly Tyr	Lys
	170 175	180
Thr Val Ser Gly	Ser Cys Met Ser Thr Gly Phe Ser Arg Ala	Val
	185 190	195
Gln Thr His Ser	Ser Lys Phe Phe Glu Glu Asp Gly Ser Leu	Lys
	200 205	210
Glu Val His Lys	Ile Asn Glu Met Tyr Ala Ser Leu Gln Glu	Glu
	215 220	225
Leu Lys Ser Ile	Cys Lys Lys Val Glu Asp Ser Glu Gln Ala	Val
	230 235	240
Asp Lys Leu Val	Lys Asp Val Asn Arg Leu Lys Arg Glu Ile	Glu
	245 250	255
Lys Arg Arg Gly	Ala Gln Ile Gln Ala Ala Arg Glu Lys Asn	Ile
	260 265	270
Gln Lys Asp Pro	Gln Glu Asn Ile Phe Leu Cys Gln Ala Leu	Arg
	275 280	285
Thr Phe Phe Pro	Asn Ser Glu Phe Leu His Ser Cys Val Met	Ser
	290 295	300
Leu Lys Asn Arg	His Val Ser Lys Ser Ser Cys Asn Tyr Asn	His
	305 310	315
His Leu Asp Val	Val Asp Asn Leu Thr Leu Met Val Glu His	Thr
	320 325	330
Asp Ile Pro Glu	Ala Ser Pro Ala Ser Thr Pro Gln Ile Ile	Lys
	335 340	345
His Lys Ala Leu	Asp Leu Asp Asp Arg Trp Gln Phe Lys Arg	Ser
	350 355	360
Arg Leu Leu Asp	Thr Gln Asp Lys Arg Ser Lys Ala Asn Thr	Gly
	365 370	375
Ser Ser Asn Gln	Asp Lys Ala Ser Lys Met Ser Ser Pro Glu	Thr
	380 385	390
Asp Glu Glu Ile	Glu Lys Met Lys Gly Phe Gly Glu Tyr Ser	Arg
	395 400	405
Ser Pro Thr Phe		

<210> 159
<211> 2651
<212> DNA
<213> Homo sapiens

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c 2651

<210> 160

<211> 556

<212> PRT

<213> Homo sapiens

<400> 160

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Leu	Ser	Ala	Ala	Leu	Leu	Ala	Ala	Glu	Leu	Lys	Ser	Lys	Ser	Cys
				20				25						30

Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn

	35	40	45
Asp Ala Pro Leu His Glu Ile Asn Gly Asp His Leu Lys Ile Cys	50	55	60
Pro Gln Gly Ser Thr Cys Cys Ser Gln Glu Met Glu Glu Lys Tyr	65	70	75
Ser Leu Gln Ser Lys Asp Asp Phe Lys Ser Val Val Ser Glu Gln	80	85	90
Cys Asn His Leu Gln Ala Val Phe Ala Ser Arg Tyr Lys Lys Phe	95	100	105
Asp Glu Phe Phe Lys Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu	110	115	120
Asn Asp Met Phe Val Lys Thr Tyr Gly His Leu Tyr Met Gln Asn	125	130	135
Ser Glu Leu Phe Lys Asp Leu Phe Val Glu Leu Lys Arg Tyr Tyr	140	145	150
Val Val Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val Asn Ser Gln Tyr	170	175	180
His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys Tyr Thr Glu	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Leu Gln	200	205	210
Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly Leu	215	220	225
Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro	230	235	240
Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser	245	250	255
His Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys	260	265	270
Ser Asn Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp	275	280	285
Phe Glu Trp Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser	320	325	330
Val Gln Val Ser Gln Lys Val Phe Gln Gly Cys Gly Pro Pro Lys	335	340	345
Pro Leu Pro Ala Gly Arg Ile Ser Arg Ser Ile Ser Glu Ser Ala			

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Phe Ser Ala Arg	Phe Arg Pro His His	Pro Glu Glu Arg Pro	Thr		
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Thr Ala Ala Gly	Thr Ser Leu Asp Arg	Leu Val Thr Asp Val	Lys		
	380	385	390		
Glu Lys Leu Lys	Gln Ala Lys Lys Phe	Trp Ser Ser Leu Pro	Ser		
	395	400	405		
Asn Val Cys Asn	Asp Glu Arg Met Ala	Ala Gly Asn Gly Asn	Glu		
	410	415	420		
Asp Asp Cys Trp	Asn Gly Lys Gly Lys	Ser Arg Tyr Leu Phe	Ala		
	425	430	435		
Val Thr Gly Asn	Gly Leu Ala Asn Gln	Gly Asn Asn Pro Glu	Val		
	440	445	450		
Gln Val Asp Thr	Ser Lys Pro Asp Ile	Leu Ile Leu Arg Gln	Ile		
	455	460	465		
Met Ala Leu Arg	Val Met Thr Ser Lys	Met Lys Asn Ala Tyr	Asn		
	470	475	480		
Gly Asn Asp Val	Asp Phe Phe Asp Ile	Ser Asp Glu Ser Ser	Gly		
	485	490	495		
Glu Gly Ser Gly	Ser Gly Cys Glu Tyr	Gln Gln Cys Pro Ser	Glu		
	500	505	510		
Phe Asp Tyr Asn	Ala Thr Asp His Ala	Gly Lys Ser Ala Asn	Glu		
	515	520	525		
Lys Ala Asp Ser	Ala Gly Val Arg Pro	Gly Ala Gln Ala Tyr	Leu		
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<210> 162
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<220>
 <223> Synthetic oligonucleotide probe

<400> 162
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<210> 163
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 164
<211> 870
<212> DNA
<213> Homo sapiens

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<210> 165
<211> 119
<212> PRT
<213> Homo sapiens

<400> 165
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	35		40		45
Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala					
	50		55		60
Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met					
	65		70		75
Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys					
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<210> 168

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 168

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<210> 169

<211> 277

<212> PRT

<213> Homo sapiens

<400> 169

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Thr	Leu	Pro	Leu	His	Leu	Met	Ala	Leu	Leu	Gly	Cys	Trp	Gln	Pro	20	25	30	
Leu	Cys	Lys	Ser	Tyr	Phe	Pro	Tyr	Leu	Met	Ala	Val	Leu	Thr	Pro	35	40	45	
Lys	Ser	Asn	Arg	Lys	Met	Glu	Ser	Lys	Lys	Arg	Glu	Leu	Phe	Ser	50	55	60	
Gln	Ile	Lys	Gly	Leu	Thr	Gly	Ala	Ser	Gly	Lys	Val	Ala	Leu	Leu	65	70	75	
Glu	Leu	Gly	Cys	Gly	Thr	Gly	Ala	Asn	Phe	Gln	Phe	Tyr	Pro	Pro	80	85	90	
Gly	Cys	Arg	Val	Thr	Cys	Leu	Asp	Pro	Asn	Pro	His	Phe	Glu	Lys	95	100	105	
Phe	Leu	Thr	Lys	Ser	Met	Ala	Glu	Asn	Arg	His	Leu	Gln	Tyr	Glu	110	115	120	
Arg	Phe	Val	Val	Ala	Pro	Gly	Glu	Asp	Met	Arg	Gln	Leu	Ala	Asp	125	130	135	
Gly	Ser	Met	Asp	Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	140	145	150	
Gln	Ser	Pro	Arg	Lys	Val	Leu	Gln	Glu	Val	Arg	Arg	Val	Leu	Arg	155	160	165	
Pro	Gly	Gly	Val	Leu	Phe	Phe	Trp	Glu	His	Val	Ala	Glu	Pro	Tyr	170	175	180	
Gly	Ser	Trp	Ala	Phe	Met	Trp	Gln	Gln	Val	Phe	Glu	Pro	Thr	Trp	185	190	195	
Lys	His	Ile	Gly	Asp	Gly	Cys	Cys	Leu	Thr	Arg	Glu	Thr	Trp	Lys	200	205	210	
Asp	Leu	Glu	Asn	Ala	Gln	Phe	Ser	Glu	Ile	Gln	Met	Glu	Arg	Gln	215	220	225	

Pro	Pro	Pro	Leu	Lys	Trp	Leu	Pro	Val	Gly	Pro	His	Ile	Met	Gly
				230					235					240
Lys	Ala	Val	Lys	Gln	Ser	Phe	Pro	Ser	Ser	Lys	Ala	Leu	Ile	Cys
				245					250					255
Ser	Phe	Pro	Ser	Leu	Gln	Leu	Glu	Gln	Ala	Thr	His	Gln	Pro	Ile
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Tyr	Leu	Pro	Leu	Arg	Gly	Thr								
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 <211> 1621
 <212> DNA
 <213> Homo sapiens

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<210> 173
<211> 1866
<212> DNA
<213> Homo sapiens

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<210> 174

<211> 823

<212> DNA

<213> Homo sapiens

<400> 174

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 gggaagcaaa ctggaaccca tggcaataat aggagggtgt ccaggctggg 750

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 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 175
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 Cys Trp Ala Cys His Ser Arg Leu Pro Thr Leu Thr Leu Ser Leu
 35 40 45
 Asn Pro Val Pro Thr Pro Ala Leu Ala Pro Val Leu Arg Arg Pro
 50 55 60
 His His Pro Arg Ser Pro Ala Met Lys Ala Ala Thr Cys Cys Ser
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 Pro Glu Gly Pro Trp Pro Ser Leu Glu Pro Arg Thr
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 <212> DNA
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 gatacaatcc ttggcctgtg tatcctcgca ttagccttgt ctttggccat 250
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<210> 177

<211> 445

<212> PRT

<213> Homo sapiens

<400> 177

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				20					25					30

Leu	Leu	Val	His	Ile	Phe	Ile	Ser	Leu	Val	Ile	Leu	Gly	Leu	Leu
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Phe	Val	Cys	Gly	Val	Leu	Trp	Trp	Leu	Tyr	Tyr	Asp	Tyr	Thr	Asn
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Asp	Leu	Ser	Ile	Glu	Leu	Asp	Thr	Glu	Arg	Glu	Asn	Met	Lys	Cys
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Val	Leu	Gly	Phe	Ala	Ile	Val	Ser	Thr	Gly	Ile	Thr	Ala	Val	Leu
				80					85					90

Leu	Val	Leu	Ile	Phe	Val	Leu	Arg	Lys	Arg	Ile	Lys	Leu	Thr	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				95					100					105
Glu	Leu	Phe	Gln	Ile 110	Thr	Asn	Lys	Ala	Ile 115	Ser	Ser	Ala	Pro	Phe 120
Leu	Leu	Phe	Gln	Pro 125	Leu	Trp	Thr	Phe	Ala 130	Ile	Leu	Ile	Phe	Phe 135
Trp	Val	Leu	Trp	Val 140	Ala	Val	Leu	Leu	Ser 145	Leu	Gly	Thr	Ala	Gly 150
Ala	Ala	Gln	Val	Met 155	Glu	Gly	Gly	Gln	Val 160	Glu	Tyr	Lys	Pro	Leu 165
Ser	Gly	Ile	Arg	Tyr 170	Met	Trp	Ser	Tyr	His 175	Leu	Ile	Gly	Leu	Ile 180
Trp	Thr	Ser	Glu	Phe 185	Ile	Leu	Ala	Cys	Gln 190	Gln	Met	Thr	Ile	Ala 195
Gly	Ala	Val	Val	Thr 200	Cys	Tyr	Phe	Asn	Arg 205	Ser	Lys	Asn	Asp	Pro 210
Pro	Asp	His	Pro	Ile 215	Leu	Ser	Ser	Leu	Ser 220	Ile	Leu	Phe	Phe	Tyr 225
His	Gln	Gly	Thr	Val 230	Val	Lys	Gly	Ser	Phe 235	Leu	Ile	Ser	Val	Val 240
Arg	Ile	Pro	Arg	Ile 245	Ile	Val	Met	Tyr	Met 250	Gln	Asn	Ala	Leu	Lys 255
Glu	Gln	Gln	His	Gly 260	Ala	Leu	Ser	Arg	Tyr 265	Leu	Phe	Arg	Cys	Cys 270
Tyr	Cys	Cys	Phe	Trp 275	Cys	Leu	Asp	Lys	Tyr 280	Leu	Leu	His	Leu	Asn 285
Gln	Asn	Ala	Tyr	Thr 290	Thr	Thr	Ala	Ile	Asn 295	Gly	Thr	Asp	Phe	Cys 300
Thr	Ser	Ala	Lys	Asp 305	Ala	Phe	Lys	Ile	Leu 310	Ser	Lys	Asn	Ser	Ser 315
His	Phe	Thr	Ser	Ile 320	Asn	Cys	Phe	Gly	Asp 325	Phe	Ile	Ile	Phe	Leu 330
Gly	Lys	Val	Leu	Val 335	Val	Cys	Phe	Thr	Val 340	Phe	Gly	Gly	Leu	Met 345
Ala	Phe	Asn	Tyr	Asn 350	Arg	Ala	Phe	Gln	Val 355	Trp	Ala	Val	Pro	Leu 360
Leu	Leu	Val	Ala	Phe 365	Phe	Ala	Tyr	Leu	Val 370	Ala	His	Ser	Phe	Leu 375
Ser	Val	Phe	Glu	Thr 380	Val	Leu	Asp	Ala	Leu 385	Phe	Leu	Cys	Phe	Ala 390
Val	Asp	Leu	Glu	Thr 395	Asn	Asp	Gly	Ser	Ser 400	Glu	Lys	Pro	Tyr	Phe 405
Met	Asp	Gln	Glu	Phe	Leu	Ser	Phe	Val	Lys	Arg	Ser	Asn	Lys	Leu

	410		415		420
Asn Asn Ala Arg	Ala Gln Gln Asp Lys His Ser Leu Arg Asn Glu				
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Glu Gly Thr Glu	Leu Gln Ala Ile Val Arg				
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<210> 178

<211> 2773

<212> DNA

<213> Homo sapiens

<400> 178

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<211> 678
 <212> PRT
 <213> Homo sapiens

<400> 179

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			20						25					30
Ala	Lys	Lys	Ile	Lys	Arg	Pro	Lys	Phe	Thr	Val	Pro	Gln	Ile	Asn
				35					40					45
Cys	Asp	Val	Lys	Ala	Gly	Lys	Ile	Ile	Asp	Pro	Glu	Phe	Ile	Val
				50					55					60
Lys	Cys	Pro	Ala	Gly	Cys	Gln	Asp	Pro	Lys	Tyr	His	Val	Tyr	Gly
				65					70					75
Thr	Asp	Val	Tyr	Ala	Ser	Tyr	Ser	Ser	Val	Cys	Gly	Ala	Ala	Val
				80					85					90
His	Ser	Gly	Val	Leu	Asp	Asn	Ser	Gly	Gly	Lys	Ile	Leu	Val	Arg
				95					100					105
Lys	Val	Ala	Gly	Gln	Ser	Gly	Tyr	Lys	Gly	Ser	Tyr	Ser	Asn	Gly
				110					115					120
Val	Gln	Ser	Leu	Ser	Leu	Pro	Arg	Trp	Arg	Glu	Ser	Phe	Ile	Val
				125					130					135
Leu	Glu	Ser	Lys	Pro	Lys	Lys	Gly	Val	Thr	Tyr	Pro	Ser	Ala	Leu
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Thr	Tyr	Ser	Ser	Ser	Lys	Ser	Pro	Ala	Ala	Gln	Ala	Gly	Glu	Thr
				155					160					165
Thr	Lys	Ala	Tyr	Gln	Arg	Pro	Pro	Ile	Pro	Gly	Thr	Thr	Ala	Gln
				170					175					180
Pro	Val	Thr	Leu	Met	Gln	Leu	Leu	Ala	Val	Thr	Val	Ala	Val	Ala
				185					190					195
Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr
				200					205					210
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu
				215					220					225
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg
				230					235					240
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala
				245					250					255
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val
				260					265					270
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu
				275					280					285
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly

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				305					310					315					
Leu	Ala	Asp	Val	Ala	Gln	Ala	Leu	Asp	Ile	Gly	Pro	Ala	Gly	Pro					
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Leu	Met	Gly	Val	Val	Gln	Tyr	Gly	Asp	Asn	Pro	Ala	Thr	His	Phe					
				335					340					345					
Asn	Leu	Lys	Thr	His	Thr	Asn	Ser	Arg	Asp	Leu	Lys	Thr	Ala	Ile					
				350					355					360					
Glu	Lys	Ile	Thr	Gln	Arg	Gly	Gly	Leu	Ser	Asn	Val	Gly	Arg	Ala					
				365					370					375					
Ile	Ser	Phe	Val	Thr	Lys	Asn	Phe	Phe	Ser	Lys	Ala	Asn	Gly	Asn					
				380					385					390					
Arg	Ser	Gly	Ala	Pro	Asn	Val	Val	Val	Val	Met	Val	Asp	Gly	Trp					
				395					400					405					
Pro	Thr	Asp	Lys	Val	Glu	Glu	Ala	Ser	Arg	Leu	Ala	Arg	Glu	Ser					
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Gly	Ile	Asn	Ile	Phe	Phe	Ile	Thr	Ile	Glu	Gly	Ala	Ala	Glu	Asn					
				425					430					435					
Glu	Lys	Gln	Tyr	Val	Val	Glu	Pro	Asn	Phe	Ala	Asn	Lys	Ala	Val					
				440					445					450					
Cys	Arg	Thr	Asn	Gly	Phe	Tyr	Ser	Leu	His	Val	Gln	Ser	Trp	Phe					
				455					460					465					
Gly	Leu	His	Lys	Thr	Leu	Gln	Pro	Leu	Val	Lys	Arg	Val	Cys	Asp					
				470					475					480					
Thr	Asp	Arg	Leu	Ala	Cys	Ser	Lys	Thr	Cys	Leu	Asn	Ser	Ala	Asp					
				485					490					495					
Ile	Gly	Phe	Val	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Thr	Gly	Asn					
				500					505					510					
Phe	Arg	Thr	Val	Leu	Gln	Phe	Val	Thr	Asn	Leu	Thr	Lys	Glu	Phe					
				515					520					525					
Glu	Ile	Ser	Asp	Thr	Asp	Thr	Arg	Ile	Gly	Ala	Val	Gln	Tyr	Thr					
				530					535					540					
Tyr	Glu	Gln	Arg	Leu	Glu	Phe	Gly	Phe	Asp	Lys	Tyr	Ser	Ser	Lys					
				545					550					555					
Pro	Asp	Ile	Leu	Asn	Ala	Ile	Lys	Arg	Val	Gly	Tyr	Trp	Ser	Gly					
				560					565					570					
Gly	Thr	Ser	Thr	Gly	Ala	Ala	Ile	Asn	Phe	Ala	Leu	Glu	Gln	Leu					
				575					580					585					
Phe	Lys	Lys	Ser	Lys	Pro	Asn	Lys	Arg	Lys	Leu	Met	Ile	Leu	Ile					
				590					595					600					
Thr	Asp	Gly	Arg	Ser	Tyr	Asp	Asp	Val	Arg	Ile	Pro	Ala	Met	Ala					

605	610	615
Ala His Leu Lys Gly Val Ile Thr Tyr	Ala Ile Gly Val Ala Trp	
620	625	630
Ala Ala Gln Glu Glu Leu Glu Val Ile	Ala Thr His Pro Ala Arg	
635	640	645
Asp His Ser Phe Phe Val Asp Glu Phe	Asp Asn Leu His Gln Tyr	
650	655	660
Val Pro Arg Ile Ile Gln Asn Ile Cys	Thr Glu Phe Asn Ser Gln	
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Pro Arg Asn

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 <211> 1759
 <212> DNA
 <213> Homo sapiens

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Tyr	Gly	Thr	Val	Asn 140	Leu	Leu	His	Gly	Val 145	Asn	Pro	Gly	Glu	Thr 150
Pro	Val	Thr	Cys	Thr 155	Ala	Gly	Ile	Gly	Thr 160	Phe	Ile	Val	Glu	Phe 165
Ala	Thr	Leu	Ser	Ser 170	Leu	Thr	Gly	Asp	Pro 175	Val	Phe	Glu	Asp	Val 180
Ala	Arg	Val	Ala	Leu 185	Met	Arg	Leu	Trp	Glu 190	Ser	Arg	Ser	Asp	Ile 195
Gly	Leu	Val	Gly	Asn 200	His	Ile	Asp	Val	Leu 205	Thr	Gly	Lys	Trp	Val 210
Ala	Gln	Asp	Ala	Gly 215	Ile	Gly	Ala	Gly	Val 220	Asp	Ser	Tyr	Phe	Glu 225
Tyr	Leu	Val	Lys	Gly 230	Ala	Ile	Leu	Leu	Gln 235	Asp	Lys	Lys	Leu	Met 240
Ala	Met	Phe	Leu	Glu 245	Tyr	Asn	Lys	Ala	Ile 250	Arg	Asn	Tyr	Thr	Arg 255
Phe	Asp	Asp	Trp	Tyr 260	Leu	Trp	Val	Gln	Met 265	Tyr	Lys	Gly	Thr	Val 270
Ser	Met	Pro	Val	Phe 275	Gln	Ser	Leu	Glu	Ala 280	Tyr	Trp	Pro	Gly	Leu 285
Gln	Ser	Leu	Ile	Gly 290	Asp	Ile	Asp	Asn	Ala 295	Met	Arg	Thr	Phe	Leu 300
Asn	Tyr	Tyr	Thr	Val 305	Trp	Lys	Gln	Phe	Gly 310	Gly	Leu	Pro	Glu	Phe 315
Tyr	Asn	Ile	Pro	Gln 320	Gly	Tyr	Thr	Val	Glu 325	Lys	Arg	Glu	Gly	Tyr 330
Pro	Leu	Arg	Pro	Glu 335	Leu	Ile	Glu	Ser	Ala 340	Met	Tyr	Leu	Tyr	Arg 345
Ala	Thr	Gly	Asp	Pro 350	Thr	Leu	Leu	Glu	Leu 355	Gly	Arg	Asp	Ala	Val 360
Glu	Ser	Ile	Glu	Lys 365	Ile	Ser	Lys	Val	Glu 370	Cys	Gly	Phe	Ala	Thr 375
Ile	Lys	Asp	Leu	Arg 380	Asp	His	Lys	Leu	Asp 385	Asn	Arg	Met	Glu	Ser 390
Phe	Phe	Leu	Ala	Glu 395	Thr	Val	Lys	Tyr	Leu 400	Tyr	Leu	Leu	Phe	Asp 405
Pro	Thr	Asn	Phe	Ile 410	His	Asn	Asn	Gly	Ser 415	Thr	Phe	Asp	Ala	Val 420
Ile	Thr	Pro	Tyr	Gly 425	Glu	Cys	Ile	Leu	Gly 430	Ala	Gly	Gly	Tyr	Ile 435
Phe	Asn	Thr	Glu	Ala	His	Pro	Ile	Asp	Leu	Ala	Ala	Leu	His	Cys

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Cys Gln Arg Leu Lys Glu Glu Gln Trp Glu Val Glu Asp Leu Met					
	455		460		465
Arg Glu Phe Tyr Ser Leu Lys Arg Ser Arg Ser Lys Phe Gln Lys					
	470		475		480
Asn Thr Val Ser Ser Gly Pro Trp Glu Pro Pro Ala Arg Pro Gly					
	485		490		495
Thr Leu Phe Ser Pro Glu Asn His Asp Gln Ala Arg Glu Arg Lys					
	500		505		510
Pro Ala Lys Gln Lys Val Pro Leu Leu Ser Cys Pro Ser Gln Pro					
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Ser					

<210> 182
 <211> 2056
 <212> DNA
 <213> Homo sapiens

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<213> Homo sapiens

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<221> N-glycosylation sites

<222> 40-43, 134-137

<223> N-glycosylation sites.

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<221> Tissue factor proteins homology

<222> 92-119

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<220>

<221> Transmembrane domain

<222> 230-255

<223> Transmembrane domain

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<221> Integrins alpha chain protein homology

<222> 232-262

<223> Integrins alpha chain protein homology

<400> 183

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35 40 45

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
50 55 60

Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
65 70 75

Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
80 85 90

Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
95 100 105

Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
110 115 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser
125 130 135

Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe
140 145 150

His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe
155 160 165

Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val
170 175 180

Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met
185 190 195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys
200 205 210

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu
215 220 225

Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
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<211> 808

<212> DNA

<213> Homo sapiens

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<221> unsure

<222> 654, 711, 748

<223> unknown base

<400> 184

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<210> 186
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<400> 186
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<210> 187
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<210> 188
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<210> 189

<211> 187

<212> PRT

<213> Homo sapiens

<400> 189

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				20					25					30
Val	Asn	Ile	Arg	Gly	Lys	Leu	Val	Ser	Leu	Glu	Lys	Tyr	Arg	Gly
				35					40					45
Ser	Val	Ser	Leu	Val	Val	Asn	Val	Ala	Ser	Glu	Cys	Gly	Phe	Thr
				50					55					60
Asp	Gln	His	Tyr	Arg	Ala	Leu	Gln	Gln	Leu	Gln	Arg	Asp	Leu	Gly
				65					70					75
Pro	His	His	Phe	Asn	Val	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly
				80					85					90
Gln	Gln	Glu	Pro	Asp	Ser	Asn	Lys	Glu	Ile	Glu	Ser	Phe	Ala	Arg
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Arg	Thr	Tyr	Ser	Val	Ser	Phe	Pro	Met	Phe	Ser	Lys	Ile	Ala	Val
				110					115					120
Thr	Gly	Thr	Gly	Ala	His	Pro	Ala	Phe	Lys	Tyr	Leu	Ala	Gln	Thr
				125					130					135
Ser	Gly	Lys	Glu	Pro	Thr	Trp	Asn	Phe	Trp	Lys	Tyr	Leu	Val	Ala
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Pro	Asp	Gly	Lys	Val	Val	Gly	Ala	Trp	Asp	Pro	Thr	Val	Ser	Val

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 <212> DNA
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<220>
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 <211> 2187
 <212> DNA
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 <211> 615
 <212> PRT
 <213> Homo sapiens

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 Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly
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 Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu Arg Glu Ala
 80 85 90
 Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala Gln Leu
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 Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile Gly
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 Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu
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 Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro Gly
 215 220 225
 Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
 230 235 240
 His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His

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Lys Gly Ala Thr	Leu Ser His Tyr Asn	Ile Val Asn Asn Ser	Asn		
	275		280		285
Ile Leu Gly Glu	Arg Leu Lys Leu His	Glu Lys Thr Pro Glu	Gln		
	290		295		300
Leu Arg Met Ile	Leu Pro Asn Pro Leu	Tyr His Cys Leu Gly	Ser		
	305		310		315
Val Ala Gly Thr	Met Met Cys Leu Met	Tyr Gly Ala Thr Leu	Ile		
	320		325		330
Leu Ala Ser Pro	Ile Phe Asn Gly Lys	Lys Ala Leu Glu Ala	Ile		
	335		340		345
Ser Arg Glu Arg	Gly Thr Phe Leu Tyr	Gly Thr Pro Thr Met	Phe		
	350		355		360
Val Asp Ile Leu	Asn Gln Pro Asp Phe	Ser Ser Tyr Asp Ile	Ser		
	365		370		375
Thr Met Cys Gly	Gly Val Ile Ala Gly	Ser Pro Ala Pro Pro	Glu		
	380		385		390
Leu Ile Arg Ala	Ile Ile Asn Lys Ile	Asn Met Lys Asp Leu	Val		
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Val Ala Tyr Gly	Thr Thr Glu Asn Ser	Pro Val Thr Phe Ala	His		
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Phe Pro Glu Asp	Thr Val Glu Gln Lys	Ala Glu Ser Val Gly	Arg		
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Ile Met Pro His	Thr Glu Ala Arg Ile	Met Asn Met Glu Ala	Gly		
	440		445		450
Thr Leu Ala Lys	Leu Asn Thr Pro Gly	Glu Leu Cys Ile Arg	Gly		
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Tyr Cys Val Met	Leu Gly Tyr Trp Gly	Glu Pro Gln Lys Thr	Glu		
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Glu Ala Val Asp	Gln Asp Lys Trp Tyr	Trp Thr Gly Asp Val	Ala		
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Thr Met Asn Glu	Gln Gly Phe Cys Lys	Ile Val Gly Arg Ser	Lys		
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Asp Met Ile Ile	Arg Gly Gly Glu Asn	Ile Tyr Pro Ala Glu	Leu		
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Glu Asp Phe Phe	His Thr His Pro Lys	Val Gln Glu Val Gln	Val		
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Val Gly Val Lys	Asp Asp Arg Met Gly	Glu Glu Ile Cys Ala	Cys		
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Ile Arg Leu Lys	Asp Gly Glu Glu Thr	Thr Val Glu Glu Ile	Lys		

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<211> 346

<212> PRT

<213> Homo sapiens

<400> 197

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Ala	Gly	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala
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<213> Homo sapiens

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Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu
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Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
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Asp Glu Phe Leu Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg
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atttgtatag aaagactgaa tagtgatg 678

Physical properties of the polymer	
Property	Value
Molecular weight (M _w)	100,000
Molecular weight (M _n)	50,000
Number-average molecular weight (M _n)	50,000
Weight-average molecular weight (M _w)	100,000
Polydispersity index (PDI)	2.0
Thermal stability (°C)	250
Thermal stability (h)	100
Thermal stability (days)	30
Thermal stability (months)	12
Thermal stability (years)	5
Thermal stability (decades)	2
Thermal stability (centuries)	1
Thermal stability (millennia)	0.5
Thermal stability (millions of years)	0.1
Thermal stability (billions of years)	0.01
Thermal stability (trillions of years)	0.001
Thermal stability (quadrillions of years)	0.0001
Thermal stability (quintillions of years)	0.00001
Thermal stability (sextillions of years)	0.000001
Thermal stability (septillions of years)	0.0000001
Thermal stability (octillions of years)	0.00000001
Thermal stability (nonillions of years)	0.000000001
Thermal stability (decillions of years)	0.0000000001
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Thermal stability (duodecillions of years)	0.000000000001
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Thermal stability (quadrdecillions of years)	0.00000000000001
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178

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Variable	Mean	SD	Min	Max
Age (years)	45.2	12.5	25	65
Gender (Male/Female)	55/45			
Marital status (Married/Single)	60/40			
Education (High school/College/Postgraduate)	30/40/30			
Occupation (Manager/Professional/Other)	20/40/40			
Income (€1000/€2000/€3000/€4000/€5000)	10/20/30/20/20			
Health status (Good/Fair/Poor)	40/30/30			
Smoking status (Smoker/Non-smoker)	20/80			
Alcohol consumption (Regular/Occasional/None)	10/40/50			
Family size (1/2/3/4/5)	10/20/30/20/20			
Health insurance (Yes/No)	90/10			
Chronic diseases (Hypertension/Diabetes/Heart disease)	20/10/10			
Physical activity (Regular/Inactive)	30/70			
Stress level (Low/Medium/High)	30/40/30			
Life satisfaction (Very satisfied/Satisfied/Unsatisfied)	20/40/40			
Healthcare utilization (Frequent/Regular/Infrequent)	10/40/50			
Healthcare costs (€0/€100/€200/€300/€400)	0/10/20/10/10			
Healthcare access (Easy/Difficult)	60/40			
Healthcare quality (Satisfied/Dissatisfied)	50/50			
Healthcare equity (Fair/Unfair)	40/60			
Healthcare sustainability (Sustainable/Unsustainable)	30/70			
Healthcare innovation (High/Low)	20/80			
Healthcare transparency (High/Low)	30/70			
Healthcare accountability (High/Low)	40/60			
Healthcare effectiveness (High/Low)	50/50			
Healthcare efficiency (High/Low)	60/40			
Healthcare safety (High/Low)	70/30			
Healthcare quality of care (High/Low)	80/20			
Healthcare patient satisfaction (High/Low)	90/10			
Healthcare patient engagement (High/Low)	80/20			
Healthcare patient empowerment (High/Low)	70/30			
Healthcare patient participation (High/Low)	60/40			
Healthcare patient advocacy (High/Low)	50/50			
Healthcare patient education (High/Low)	40/60			
Healthcare patient information (High/Low)	30/70			
Healthcare patient communication (High/Low)	20/80			
Healthcare patient relationship (High/Low)	10/90			
Healthcare patient trust (High/Low)	0/100			
Healthcare patient loyalty (High/Low)	0/100			
Healthcare patient retention (High/Low)	0/100			
Healthcare patient churn (High/Low)	0/100			
Healthcare patient acquisition (High/Low)	0/100			
Healthcare patient growth (High/Low)	0/100			
Healthcare patient profitability (High/Low)	0/100			
Healthcare patient ROI (High/Low)	0/100			
Healthcare patient NPS (High/Low)	0/100			
Healthcare patient CSAT (High/Low)	0/100			
Healthcare patient CES (High/Low)	0/100			
Healthcare patient KPI (High/Low)	0/100			
Healthcare patient benchmark (High/Low)	0/100			
Healthcare patient target (High/Low)	0/100			
Healthcare patient strategy (High/Low)	0/100			
Healthcare patient plan (High/Low)	0/100			
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Healthcare patient result (High/Low)	0/100			
Healthcare patient impact (High/Low)	0/100			
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Healthcare patient benefit (High/Low)	0/100			
Healthcare patient cost (High/Low)	0/100			
Healthcare patient risk (High/Low)	0/100			
Healthcare patient opportunity (High/Low)	0/100			
Healthcare patient challenge (High/Low)	0/100			
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Healthcare patient problem (High/Low)	0/100			
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Healthcare patient concern (High/Low)	0/100			
Healthcare patient complaint (High/Low)	0/100			
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Healthcare patient improvement (High/Low)	0/100			
Healthcare patient change (High/Low)	0/100			
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Healthcare patient growth (High/Low)	0/100			
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Healthcare patient diversification (High/Low)	0/100			
Healthcare patient vertical integration (High/Low)	0/100			
Healthcare patient horizontal integration (High/Low)	0/100			
Healthcare patient conglomerate (High/Low)	0/100			
Healthcare patient joint venture (High/Low)	0/100			
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[illegible]

182

<213> Homo sapiens

<400> 208

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Asp	Thr	Asn	Leu	Phe	Phe	Leu	Tyr	Arg	Ile	His	Leu	Asp	Val	Cys
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Gln	Leu	Arg	Arg	Val	Ile	Ala	Ala	His	Gly	Phe	Ser	Ser	Lys	Glu
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Tyr

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<210> 213

<211> 299

<212> PRT

<213> Homo sapiens

<400> 213

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Gln	Ile	Pro	Leu	Pro	Thr	Arg	Pro	His	Trp	Phe	Leu	Leu	Phe	Gly
				35					40					45
Thr	Thr	Glu	Glu	Glu	Ile	Gln	Glu	Ile	Cys	Ile	Glu	Thr	Leu	Arg
				50					55					60
Leu	Tyr	Thr	Arg	Lys	Lys	Pro	Asn	Tyr	Glu	Leu	Leu	Glu	Lys	Glu
				65					70					75
Val	Glu	Lys	Arg	Lys	Val	Ala	Leu	Gln	Glu	Ala	Lys	Leu	Lys	Ala
				80					85					90
Lys	Gly	Leu	Asn	Pro	Asp	Gly	Thr	Pro	Ala	Leu	Ser	Thr	Leu	Gly
				95					100					105
Gly	Phe	Ser	Pro	Ala	Ser	Lys	Pro	Ser	Ser	Pro	Arg	Glu	Val	Lys
				110					115					120
Ala	Glu	Glu	Lys	Ser	Pro	Ile	Ser	Ile	Asn	Val	Lys	Thr	Val	Lys
				125					130					135
Lys	Glu	Pro	Glu	Asp	Arg	Gln	Gln	Ala	Ser	Lys	Ser	Pro	Tyr	Asn
				140					145					150
Gly	Val	Arg	Lys	Asp	Ser	Lys	Arg	Ser	Arg	Asn	Ser	Arg	Ser	Ala
				155					160					165
Ser	Arg	Ser	Arg	Ser	Arg	Thr	Arg	Ser	Arg	Ser	Arg	Ser	His	Thr
				170					175					180
Pro	Arg	Arg	His	Tyr	Asn	Asn	Arg	Arg	Ser	Arg	Ser	Gly	Thr	Tyr
				185					190					195
Ser	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	His	Ser	Glu	Ser	Pro
				200					205					210
Arg	Arg	His	His	Asn	His	Gly	Ser	Pro	His	Leu	Lys	Ala	Lys	His
				215					220					225
Thr	Arg	Asp	Asp	Leu	Lys	Ser	Ser	Asn	Arg	His	Gly	His	Lys	Arg
				230					235					240
Lys	Lys	Ser	Arg	Ser	Arg	Ser	Gln	Ser	Lys	Ser	Arg	Asp	His	Ser
				245					250					255
Asp	Ala	Ala	Lys	Lys	His	Arg	His	Glu	Arg	Gly	His	His	Arg	Asp
				260					265					270
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His His Gly Gly Ser Arg Ser Gly His Gly Arg His Arg Arg
290 295

<210> 214
<211> 730
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663
<223> unknown base

<400> 214
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agaactgggtt tgtttcatg caagcttata gttgaaatat ttttcaggaa 400
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<211> 1807
<212> DNA
<213> Homo sapiens

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 gcagtgggtg gctctgtgct ggggtgccttc ctcaccttcc caggcctgcg 800
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<210> 216

<211> 479
 <212> PRT
 <213> Homo sapiens

<400> 216

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				20					25					30	
Leu	Leu	Cys	Asn	Gly	Ser	Leu	Phe	Arg	Tyr	Lys	His	Pro	Ser	Glu	
				35					40					45	
Glu	Glu	Leu	Arg	Ala	Leu	Ala	Gly	Lys	Pro	Arg	Pro	Arg	Gly	Arg	
				50					55					60	
Lys	Glu	Arg	Trp	Ala	Asn	Gly	Leu	Ser	Glu	Glu	Lys	Pro	Leu	Ser	
				65					70					75	
Val	Pro	Arg	Asp	Ala	Pro	Phe	Gln	Leu	Glu	Thr	Cys	Pro	Leu	Thr	
				80					85					90	
Thr	Val	Asp	Ala	Leu	Val	Leu	Arg	Phe	Phe	Leu	Glu	Tyr	Gln	Trp	
				95					100					105	
Phe	Val	Asp	Phe	Ala	Val	Tyr	Ser	Gly	Gly	Val	Tyr	Leu	Phe	Thr	
				110					115					120	
Glu	Ala	Tyr	Tyr	Tyr	Met	Leu	Gly	Pro	Ala	Lys	Glu	Thr	Asn	Ile	
				125					130					135	
Ala	Val	Phe	Trp	Cys	Leu	Leu	Thr	Val	Thr	Phe	Ser	Ile	Lys	Met	
				140					145					150	
Phe	Leu	Thr	Val	Thr	Arg	Leu	Tyr	Phe	Ser	Ala	Glu	Glu	Gly	Gly	
				155					160					165	
Glu	Arg	Ser	Val	Cys	Leu	Thr	Phe	Ala	Phe	Leu	Phe	Leu	Leu	Leu	
				170					175					180	
Ala	Met	Leu	Val	Gln	Val	Val	Arg	Glu	Glu	Thr	Leu	Glu	Leu	Gly	
				185					190					195	
Leu	Glu	Pro	Gly	Leu	Ala	Ser	Met	Thr	Gln	Asn	Leu	Glu	Pro	Leu	
				200					205					210	
Leu	Lys	Lys	Gln	Gly	Trp	Asp	Trp	Ala	Leu	Pro	Val	Ala	Lys	Leu	
				215					220					225	
Ala	Ile	Arg	Val	Gly	Leu	Ala	Val	Val	Gly	Ser	Val	Leu	Gly	Ala	
				230					235					240	
Phe	Leu	Thr	Phe	Pro	Gly	Leu	Arg	Leu	Ala	Gln	Thr	His	Arg	Asp	
				245					250					255	
Ala	Leu	Thr	Met	Ser	Glu	Asp	Arg	Pro	Met	Leu	Gln	Phe	Leu	Leu	
				260					265					270	
His	Thr	Ser	Phe	Leu	Ser	Pro	Leu	Phe	Ile	Leu	Trp	Leu	Trp	Thr	
				275					280					285	
Lys	Pro	Ile	Ala	Arg	Asp	Phe	Leu	His	Gln	Pro	Pro	Phe	Gly	Glu	

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Thr Arg Phe Ser	Leu Leu Ser Asp Ser	Ala Phe Asp Ser Gly	Arg
	305	310	315
Leu Trp Leu Leu	Val Val Leu Cys Leu	Leu Arg Leu Ala Val	Thr
	320	325	330
Arg Pro His Leu	Gln Ala Tyr Leu Cys	Leu Ala Lys Ala Arg	Val
	335	340	345
Glu Gln Leu Arg	Arg Glu Ala Gly Arg	Ile Glu Ala Arg Glu	Ile
	350	355	360
Gln Gln Arg Val	Val Arg Val Tyr Cys	Tyr Val Thr Val Val	Ser
	365	370	375
Leu Gln Tyr Leu	Thr Pro Leu Ile Leu	Thr Leu Asn Cys Thr	Leu
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Leu Leu Lys Thr	Leu Gly Gly Tyr Ser	Trp Gly Leu Gly Pro	Ala
	395	400	405
Pro Leu Leu Ser	Pro Asp Pro Ser Ser	Ala Ser Ala Ala Pro	Ile
	410	415	420
Gly Ser Gly Glu	Asp Glu Val Gln Gln	Thr Ala Ala Arg Ile	Ala
	425	430	435
Gly Ala Leu Gly	Gly Leu Leu Thr Pro	Leu Phe Leu Arg Gly	Val
	440	445	450
Leu Ala Tyr Leu	Ile Trp Trp Thr Ala	Ala Cys Gln Leu Leu	Ala
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<210> 217

<211> 574

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 5, 146

<223> unknown base

<400> 217

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<210> 218

<211> 2571

<212> DNA

<213> Homo sapiens

<400> 218

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aaatatTTTT cagaagttaa a 2571

<210> 219

<211> 632

<212> PRT

<213> Homo sapiens

<400> 219

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 <211> 773
 <212> DNA
 <213> Homo sapiens

<400> 220
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 gtttttaaca tcatcagccc aagcaacaat ggtggcaatg ttcaggagac 200
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 gatcatgotc ttctaccaca atttttgact ataaacatgg ctacattgca 300
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<210> 221
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 221
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 35 40 45
 Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser
 50 55 60
 Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val
 65 70 75
 Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn
 80 85 90

Ile	Pro	Pro	Leu	Asn	Asn	Leu	Gln	Trp	Tyr	Ile	Tyr	Glu	Lys	Gln
				95					100					105
Ala	Leu	Asp	Asn	Met	Phe	Ser	Asn	Lys	Tyr	Thr	Trp	Val	Lys	Tyr
				110					115					120
Asn	Pro	Leu	Glu	Ser	Leu	Ile	Lys	Asp	Val	Asp	Trp	Phe	Leu	Leu
				125					130					135
Gly	Ser	Pro	Ile	Glu	Lys	Leu	Cys	Lys	His	Ile	Pro	Leu	Tyr	Lys
				140					145					150
Gly	Glu	Val	Val	Glu	Asn	Thr	His	Asn	Val	Gly	Ala	Gly	Gly	Cys
				155					160					165
Ala	Lys	Ala	Gly	Leu	Leu	Gly	Ile	Leu	Gly	Ile	Ser	Ile	Cys	Ala
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Asp Ile His Val

<210> 222
 <211> 992
 <212> DNA
 <213> Homo sapiens

<400> 222
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<210> 224
<211> 1297
<212> DNA
<213> Homo sapiens

<400> 224
ggtccttaat ggcagcagcc gccgctacca agatccttct gtgcctccc 50
cttctgtctc tgctgtccgg ctggccccgg gctgggagag ccgaccctca 100
ctctctttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150
ggtggtgtgc ggttcaaggc caggtggatg aaaagacttt tcttcactat 200
gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250
aaatgtcaca acggcctgga aagcacagaa ccagtgactg agagaggtgg 300
tggacatact tacagagcaa ctgcgtgaca ttcagctgga gaattacaca 350
cccaaggaac cctcaccct gcaggcaagg atgtcttctg agcagaaagc 400
tgaaggacac agcagtggat cttggcagtt cagtttcgat gggcagatct 450
tcctcctctt tgactcagag aagagaatgt ggacaacggg tcatcctgga 500
gccagaaaga tgaaagaaaa gtgggagaat gacaagggtg tggccatgtc 550
cttccattac ttctcaatgg gagactgtat aggatggctt gaggacttct 600
tgatgggcat ggacagcacc ctggagccaa gtgcaggagc accactcgcc 650
atgtcctcag gcacaacca actcagggcc acagccacca cctcatcct 700
ttgctgcctc ctcatcatcc tcccctgctt catcctccct ggcatctgag 750
gagagtcctt tagagtgaca ggttaaagct gataccaaaa ggctcctgtg 800
agcacggtct tgatcaaact cgcccttctg tctggccagc tgcccacgac 850
ctacggtgta tgtccagtgg cctccagcag atcatgatga catcatggac 900
ccaatagctc attcactgcc ttgattcctt ttgccaacaa ttttaccagc 950
agttatacct aacatattat gcaattttct cttggtgcta cctgatggaa 1000
ttcctgcact taaagttctg gctgactaaa caagatatat cattttcttt 1050
cttctctttt tgtttgaaa atcaagtact tctttgaatg atgatctctt 1100
tcttgcaa at gatattgtca gtaaaataat cacgttagac ttcagacctc 1150
tggggattct ttccgtgtcc tgaaagagaa tttttaaat atttaataag 1200
aaaaaattta tattaatgat tgtttccttt agtaatttat tgttctgtac 1250
tgatatttaa ataaagagtt ctatttccca aaaaaaaaa aaaaaaa 1297

<210> 225
<211> 246
<212> PRT
<213> Homo sapiens

<400> 225

Met Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu
1 5 10 15
Leu Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro
20 25 30
His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro
35 40 45
Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
50 55 60
Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser
65 70 75
Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
80 85 90
Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
95 100 105
Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr
110 115 120
Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser
125 130 135
Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu
140 145 150
Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala
155 160 165
Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met
170 175 180
Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu
185 190 195
Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly
200 205 210
Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr
215 220 225
Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
230 235 240
Phe Ile Leu Pro Gly Ile
245

<210> 226

<211> 735

<212> DNA

<213> Homo sapiens

<400> 226

gggaaagcca ttctgaaaac ccatctatac aaactatata ttttcatttc 50
tgctgctagc tgccttgggc ctcaaatctt tcattctgtt ttctgacttt 100
caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

ggttttaatt ttggtggtag ccctcaccca attctggtgt ggctttcttt 200
 gcagaggatt ccaccttcaa aatcatgaac tctggctgtt gatcaaaaga 250
 gaatttggtat tctactctaa aagtcaatat aggacttggc aaaagaagct 300
 agcagaagac tcaacctggc ctcccataaa caggacagat tattcaggtg 350
 atggcaaaaa tggattctac atcaacggag gctatgaaag ccatgaacag 400
 attccaaaaa gaaaactcaa attgggaggc caaccacag aacagcattt 450
 ctgggccagg ctgtaatcag aattgtgctc gtacatgctc aacagcattg 500
 cttttttccc caaaattaac acattgtgga gaagtgatga tactctcccc 550
 ttacctttcc tctctccatt caagcattca aagtatatatt tcaatgaatt 600
 aaaccttgca gcaagggacc ttagataggc ttattctgac tgtatgcttt 650
 accaatgaga gaaaaaaatg catttcctgt atcatccttt tcaataaact 700
 gtattcattt tgaaaaaaaa aaaaaaaaaa aaaaa 735

<210> 227
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 227
 Met Glu Leu Ile Pro Thr Ile Thr Ser Trp Arg Val Leu Ile Leu
 1 5 10 15
 Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly
 20 25 30
 Phe His Leu Gln Asn His Glu Leu Trp Leu Leu Ile Lys Arg Glu
 35 40 45
 Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys
 50 55 60
 Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr
 65 70 75
 Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu
 80 85 90
 Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Gln
 95 100 105
 Pro Thr Glu Gln His Phe Trp Ala Arg Leu
 110 115

<210> 228
 <211> 2185
 <212> DNA
 <213> Homo sapiens

<400> 228
 gttctccttt ccgagccaaa atcccaggcg atggtgaatt atgaacgtgc 50
 cacaccatga agctcttggtg gcaggtaact gtgcaccacc acacctggaa 100

185										190					195				
Phe	Asn	Leu	Lys	Tyr	Leu	Asn	Leu	Gly	Met	Cys	Asn	Ile	Lys	Asp					
				200					205					210					
Met	Pro	Asn	Leu	Thr	Pro	Leu	Val	Gly	Leu	Glu	Glu	Leu	Glu	Met					
				215					220					225					
Ser	Gly	Asn	His	Phe	Pro	Glu	Ile	Arg	Pro	Gly	Ser	Phe	His	Gly					
				230					235					240					
Leu	Ser	Ser	Leu	Lys	Lys	Leu	Trp	Val	Met	Asn	Ser	Gln	Val	Ser					
				245					250					255					
Leu	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Gly	Leu	Ala	Ser	Leu	Val	Glu					
				260					265					270					
Leu	Asn	Leu	Ala	His	Asn	Asn	Leu	Ser	Ser	Leu	Pro	His	Asp	Leu					
				275					280					285					
Phe	Thr	Pro	Leu	Arg	Tyr	Leu	Val	Glu	Leu	His	Leu	His	His	Asn					
				290					295					300					
Pro	Trp	Asn	Cys	Asp	Cys	Asp	Ile	Leu	Trp	Leu	Ala	Trp	Trp	Leu					
				305					310					315					
Arg	Glu	Tyr	Ile	Pro	Thr	Asn	Ser	Thr	Cys	Cys	Gly	Arg	Cys	His					
				320					325					330					
Ala	Pro	Met	His	Met	Arg	Gly	Arg	Tyr	Leu	Val	Glu	Val	Asp	Gln					
				335					340					345					
Ala	Ser	Phe	Gln	Cys	Ser	Ala	Pro	Phe	Ile	Met	Asp	Ala	Pro	Arg					
				350					355					360					
Asp	Leu	Asn	Ile	Ser	Glu	Gly	Arg	Met	Ala	Glu	Leu	Lys	Cys	Arg					
				365					370					375					
Thr	Pro	Pro	Met	Ser	Ser	Val	Lys	Trp	Leu	Leu	Pro	Asn	Gly	Thr					
				380					385					390					
Val	Leu	Ser	His	Ala	Ser	Arg	His	Pro	Arg	Ile	Ser	Val	Leu	Asn					
				395					400					405					
Asp	Gly	Thr	Leu	Asn	Phe	Ser	His	Val	Leu	Leu	Ser	Asp	Thr	Gly					
				410					415					420					
Val	Tyr	Thr	Cys	Met	Val	Thr	Asn	Val	Ala	Gly	Asn	Ser	Asn	Ala					
				425					430					435					
Ser	Ala	Tyr	Leu	Asn	Val	Ser	Thr	Ala	Glu	Leu	Asn	Thr	Ser	Asn					
				440					445					450					
Tyr	Ser	Phe	Phe	Thr	Thr	Val	Thr	Val	Glu	Thr	Thr	Glu	Ile	Ser					
				455					460					465					
Pro	Glu	Asp	Thr	Thr	Arg	Lys	Tyr	Lys	Pro	Val	Pro	Thr	Thr	Ser					
				470					475					480					
Thr	Gly	Tyr	Gln	Pro	Ala	Tyr	Thr	Thr	Ser	Thr	Thr	Val	Leu	Ile					
				485					490					495					
Gln	Thr	Thr	Arg	Val	Pro	Lys	Gln	Val	Ala	Val	Pro	Ala	Thr	Asp					

500	505	510
Thr Thr Asp Lys Met Gln Thr Ser Leu	Asp Glu Val Met Lys Thr	
515	520	525
Thr Lys Ile Ile Ile Gly Cys Phe Val	Ala Val Thr Leu Leu Ala	
530	535	540
Ala Ala Met Leu Ile Val Phe Tyr Lys	Leu Arg Lys Arg His Gln	
545	550	555
Gln Arg Ser Thr Val Thr Ala Ala Arg	Thr Val Glu Ile Ile Gln	
560	565	570
Val Asp Glu Asp Ile Pro Ala Ala Thr	Ser Ala Ala Ala Thr Ala	
575	580	585
Ala Pro Ser Gly Val Ser Gly Glu Gly	Ala Val Val Leu Pro Thr	
590	595	600
Ile His Asp His Ile Asn Tyr Asn Thr	Tyr Lys Pro Ala His Gly	
605	610	615
Ala His Trp Thr Glu Asn Ser Leu Gly	Asn Ser Leu His Pro Thr	
620	625	630
Val Thr Thr Ile Ser Glu Pro Tyr Ile	Ile Gln Thr His Thr Lys	
635	640	645
Asp Lys Val Gln Glu Thr Gln Ile		
650		

<210> 230

<211> 2846

<212> DNA

<213> Homo sapiens

<400> 230

cgctcgggca ccagccgcgg caaggatgga gctgggttgc tggacgcagt 50

tggggctcac ttttcttcag ctcttctca tctcgtcctt gccagagag 100

tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150

tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200

gggaagtcgt gggttatacc atcccttgct gcaggaatga ggagaatgag 250

tgtgactcct gcctgatcca cccaggttgt accatctttg aaaactgcaa 300

gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga 350

aggggttcta ctgtgcagag tgccgagcag gctgggtacgg aggagactgc 400

atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450

aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg 500

ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550

atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600

ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

His	Lys	Gly	Ala	Trp	Phe	Leu	Val	Cys	Ser	Gly	Ala	Leu	Val	Asn	485	490	495
Glu	Arg	Thr	Val	Val	Val	Ala	Ala	His	Cys	Val	Thr	Asp	Leu	Gly	500	505	510
Lys	Val	Thr	Met	Ile	Lys	Thr	Ala	Asp	Leu	Lys	Val	Val	Leu	Gly	515	520	525
Lys	Phe	Tyr	Arg	Asp	Asp	Asp	Arg	Asp	Glu	Lys	Thr	Ile	Gln	Ser	530	535	540
Leu	Gln	Ile	Ser	Ala	Ile	Ile	Leu	His	Pro	Asn	Tyr	Asp	Pro	Ile	545	550	555
Leu	Leu	Asp	Ala	Asp	Ile	Ala	Ile	Leu	Lys	Leu	Leu	Asp	Lys	Ala	560	565	570
Arg	Ile	Ser	Thr	Arg	Val	Gln	Pro	Ile	Cys	Leu	Ala	Ala	Ser	Arg	575	580	585
Asp	Leu	Ser	Thr	Ser	Phe	Gln	Glu	Ser	His	Ile	Thr	Val	Ala	Gly	590	595	600
Trp	Asn	Val	Leu	Ala	Asp	Val	Arg	Ser	Pro	Gly	Phe	Lys	Asn	Asp	605	610	615
Thr	Leu	Arg	Ser	Gly	Val	Val	Ser	Val	Val	Asp	Ser	Leu	Leu	Cys	620	625	630
Glu	Glu	Gln	His	Glu	Asp	His	Gly	Ile	Pro	Val	Ser	Val	Thr	Asp	635	640	645
Asn	Met	Phe	Cys	Ala	Ser	Trp	Glu	Pro	Thr	Ala	Pro	Ser	Asp	Ile	650	655	660
Cys	Thr	Ala	Glu	Thr	Gly	Gly	Ile	Ala	Ala	Val	Ser	Phe	Pro	Gly	665	670	675
Arg	Ala	Ser	Pro	Glu	Pro	Arg	Trp	His	Leu	Met	Gly	Leu	Val	Ser	680	685	690
Trp	Ser	Tyr	Asp	Lys	Thr	Cys	Ser	His	Arg	Leu	Ser	Thr	Ala	Phe	695	700	705
Thr	Lys	Val	Leu	Pro	Phe	Lys	Asp	Trp	Ile	Glu	Arg	Asn	Met	Lys	710	715	720

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

aggttcgtga tggagacaac cgcg 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 233
tgtcaaggac gcactgccgt catg 24

<210> 234
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 234
tggccagatc atcaagcgtg tctgtggcaa cgagcggcca gtcctatcc 50

<210> 235
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 235
accaggcatt gtatcttcag ttgtcatcaa gttcgcaatc agattggaaa 50
agctcaactt gaagctttct tgctgcagt gaagcagaga gatagatatt 100
attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta 150
caaattccga ttactgttgc tgttgacttt gtgcttgaca gtgggtgggt 200
gggccaccag taactacttc gtgggtgccca ttcaagagat tcctaaagca 250
aaggagttca tggctaattt ccataagacc ctcatTTTgg ggaagggaaa 300
aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc 350
cttctgtgtc tccttacctc agaggccaga gcaagctcat tttcaaacca 400
gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg 450
ccggtatcgc ctcaggaat gtaaagcttt acagaggggt gccatctcgt 500
ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg 550
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca 600
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atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat 700
gtggacctgg taccgagaa tgactttaac ctttacaagt gtgaggagca 750
tcccaagcat ctgggtggtt gcaggaacag cactgggtac aggttacgtt 800
acagtggata ttttgggggt gttactgcc taagcagaga gcagtTTTTc 850
aagggtgaatg gattctctaa caactactgg ggatggggag gcgaagacga 900
tgacctcaga ctcagggtt agctccaaag aatgaaaatt tcccgcccc 950
tgctgaagt gggtaaatat acaatgttct tccacactag agacaaaggc 1000

aatgaggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt 1050
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aacacaatcc tttatatatc aacatcacag tggatttctg gtttggtgca 1150
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acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag 1300
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cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt 1850
tgtaaaatga ttttgtacaa gtaggatatg aattagcagt ttacaagttt 1900
acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaat 1950
gtgaaaaagc aaaa 1964

<210> 236

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> Signal peptide

<222> 1-27

<223> Signal peptide

<220>

<221> N-glycosylation sites

<222> 4-7, 220-223, 335-338

<223> N-glycosylation sites

<220>

<221> Xylose isomerase proteins

<222> 191-201

<223> Xylose isomerase proteins

<400> 236

Met	Gly	Phe	Asn	Leu	Thr	Phe	His	Leu	Ser	Tyr	Lys	Phe	Arg	Leu
1					5					10				15

Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr	
				20					25					30	
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys	
				35					40					45	
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly	
				50					55					60	
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp	
				65					70					75	
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu	
				80					85					90	
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn	
				95					100					105	
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala	
				110					115					120	
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys	
				125					130					135	
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg	
				140					145					150	
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly	
				155					160					165	
Lys	Lys	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu	
				170					175					180	
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val	
				185					190					195	
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu	
				200					205					210	
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg	
				215					220					225	
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg	
				230					235					240	
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly	
				245					250					255	
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Gln	
				260					265					270	
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr	
				275					280					285	
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu	
				290					295					300	
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp	
				305					310					315	
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn	
				320					325					330	

1. <i>Staphylococcus aureus</i>		2. <i>Staphylococcus aureus</i>		3. <i>Staphylococcus aureus</i>		4. <i>Staphylococcus aureus</i>		5. <i>Staphylococcus aureus</i>		6. <i>Staphylococcus aureus</i>		7. <i>Staphylococcus aureus</i>		8. <i>Staphylococcus aureus</i>		9. <i>Staphylococcus aureus</i>		10. <i>Staphylococcus aureus</i>		11. <i>Staphylococcus aureus</i>		12. <i>Staphylococcus aureus</i>		13. <i>Staphylococcus aureus</i>		14. <i>Staphylococcus aureus</i>		15. <i>Staphylococcus aureus</i>		16. <i>Staphylococcus aureus</i>		17. <i>Staphylococcus aureus</i>		18. <i>Staphylococcus aureus</i>		19. <i>Staphylococcus aureus</i>		20. <i>Staphylococcus aureus</i>		21. <i>Staphylococcus aureus</i>		22. <i>Staphylococcus aureus</i>		23. <i>Staphylococcus aureus</i>		24. <i>Staphylococcus aureus</i>		25. <i>Staphylococcus aureus</i>		26. <i>Staphylococcus aureus</i>		27. <i>Staphylococcus aureus</i>		28. <i>Staphylococcus aureus</i>		29. <i>Staphylococcus aureus</i>		30. <i>Staphylococcus aureus</i>		31. <i>Staphylococcus aureus</i>		32. <i>Staphylococcus aureus</i>		33. <i>Staphylococcus aureus</i>		34. <i>Staphylococcus aureus</i>		35. <i>Staphylococcus aureus</i>		36. <i>Staphylococcus aureus</i>		37. <i>Staphylococcus aureus</i>		38. <i>Staphylococcus aureus</i>		39. <i>Staphylococcus aureus</i>		40. <i>Staphylococcus aureus</i>		41. <i>Staphylococcus aureus</i>		42. <i>Staphylococcus aureus</i>		43. <i>Staphylococcus aureus</i>		44. <i>Staphylococcus aureus</i>		45. <i>Staphylococcus aureus</i>		46. <i>Staphylococcus aureus</i>		47. <i>Staphylococcus aureus</i>		48. <i>Staphylococcus aureus</i>		49. <i>Staphylococcus aureus</i>		50. <i>Staphylococcus aureus</i>		51. <i>Staphylococcus aureus</i>		52. <i>Staphylococcus aureus</i>		53. <i>Staphylococcus aureus</i>		54. <i>Staphylococcus aureus</i>		55. <i>Staphylococcus aureus</i>		56. <i>Staphylococcus aureus</i>		57. <i>Staphylococcus aureus</i>		58. <i>Staphylococcus aureus</i>		59. <i>Staphylococcus aureus</i>		60. <i>Staphylococcus aureus</i>		61. <i>Staphylococcus aureus</i>		62. <i>Staphylococcus aureus</i>		63. <i>Staphylococcus aureus</i>		64. <i>Staphylococcus aureus</i>		65. <i>Staphylococcus aureus</i>		66. <i>Staphylococcus aureus</i>		67. <i>Staphylococcus aureus</i>		68. <i>Staphylococcus aureus</i>		69. <i>Staphylococcus aureus</i>		70. <i>Staphylococcus aureus</i>		71. <i>Staphylococcus aureus</i>		72. <i>Staphylococcus aureus</i>		73. <i>Staphylococcus aureus</i>		74. <i>Staphylococcus aureus</i>		75. <i>Staphylococcus aureus</i>		76. <i>Staphylococcus aureus</i>		77. <i>Staphylococcus aureus</i>		78. <i>Staphylococcus aureus</i>		79. <i>Staphylococcus aureus</i>		80. <i>Staphylococcus aureus</i>		81. <i>Staphylococcus aureus</i>		82. <i>Staphylococcus aureus</i>		83. <i>Staphylococcus aureus</i>		84. <i>Staphylococcus aureus</i>		85. <i>Staphylococcus aureus</i>		86. <i>Staphylococcus aureus</i>		87. <i>Staphylococcus aureus</i>		88. <i>Staphylococcus aureus</i>		89. <i>Staphylococcus aureus</i>		90. <i>Staphylococcus aureus</i>		91. <i>Staphylococcus aureus</i>		92. <i>Staphylococcus aureus</i>		93. <i>Staphylococcus aureus</i>		94. <i>Staphylococcus aureus</i>		95. <i>Staphylococcus aureus</i>		96. <i>Staphylococcus aureus</i>		97. <i>Staphylococcus aureus</i>		98. <i>Staphylococcus aureus</i>		99. <i>Staphylococcus aureus</i>		100. <i>Staphylococcus aureus</i>	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																																																																																																				

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 acgcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcacgaga 2350
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 agctactcgg gaggctgagg caggagaatg gtgcgaaccc gggaggcgga 2500
 gcttgcaagt agcccagatg gcgccactgc actccagcct gagtgcaga 2550
 gcgagactct gtctcca 2567

<210> 241

<211> 423

<212> PRT

<213> Homo sapiens

<400> 241

Met	Ala	Gln	Ala	Val	Trp	Ser	Arg	Leu	Gly	Arg	Ile	Leu	Trp	Leu	1	5	10	15
Ala	Cys	Leu	Leu	Pro	Trp	Ala	Pro	Ala	Gly	Val	Ala	Ala	Gly	Leu	20	25	30	
Tyr	Glu	Leu	Asn	Leu	Thr	Thr	Asp	Ser	Pro	Ala	Thr	Thr	Gly	Ala	35	40	45	
Val	Val	Thr	Ile	Ser	Ala	Ser	Leu	Val	Ala	Lys	Asp	Asn	Gly	Ser	50	55	60	
Leu	Ala	Leu	Pro	Ala	Asp	Ala	His	Leu	Tyr	Arg	Phe	His	Trp	Ile	65	70	75	
His	Thr	Pro	Leu	Val	Leu	Thr	Gly	Lys	Met	Glu	Lys	Gly	Leu	Ser	80	85	90	
Ser	Thr	Ile	Arg	Val	Val	Gly	His	Val	Pro	Gly	Glu	Phe	Pro	Val	95	100	105	
Ser	Val	Trp	Val	Thr	Ala	Ala	Asp	Cys	Trp	Met	Cys	Gln	Pro	Val	110	115	120	
Ala	Arg	Gly	Phe	Val	Val	Leu	Pro	Ile	Thr	Glu	Phe	Leu	Val	Gly	125	130	135	
Asp	Leu	Val	Val	Thr	Gln	Asn	Thr	Ser	Leu	Pro	Trp	Pro	Ser	Ser	140	145	150	
Tyr	Leu	Thr	Lys	Thr	Val	Leu	Lys	Val	Ser	Phe	Leu	Leu	His	Asp	155	160	165	
Pro	Ser	Asn	Phe	Leu	Lys	Thr	Ala	Leu	Phe	Leu	Tyr	Ser	Trp	Asp	170	175	180	
Phe	Gly	Asp	Gly	Thr	Gln	Met	Val	Thr	Glu	Asp	Ser	Val	Val	Tyr	185	190	195	

Tyr	Asn	Tyr	Ser	Ile	Ile	Gly	Thr	Phe	Thr	Val	Lys	Leu	Lys	Val
				200					205					210
Val	Ala	Glu	Trp	Glu	Glu	Val	Glu	Pro	Asp	Ala	Thr	Arg	Ala	Val
				215					220					225
Lys	Gln	Lys	Thr	Gly	Asp	Phe	Ser	Ala	Ser	Leu	Lys	Leu	Gln	Glu
				230					235					240
Thr	Leu	Arg	Gly	Ile	Gln	Val	Leu	Gly	Pro	Thr	Leu	Ile	Gln	Thr
				245					250					255
Phe	Gln	Lys	Met	Thr	Val	Thr	Leu	Asn	Phe	Leu	Gly	Ser	Pro	Pro
				260					265					270
Leu	Thr	Val	Cys	Trp	Arg	Leu	Lys	Pro	Glu	Cys	Leu	Pro	Leu	Glu
				275					280					285
Glu	Gly	Glu	Cys	His	Pro	Val	Ser	Val	Ala	Ser	Thr	Ala	Tyr	Asn
				290					295					300
Leu	Thr	His	Thr	Phe	Arg	Asp	Pro	Gly	Asp	Tyr	Cys	Phe	Ser	Ile
				305					310					315
Arg	Ala	Glu	Asn	Ile	Ile	Ser	Lys	Thr	His	Gln	Tyr	His	Lys	Ile
				320					325					330
Gln	Val	Trp	Pro	Ser	Arg	Ile	Gln	Pro	Ala	Val	Phe	Ala	Phe	Pro
				335					340					345
Cys	Ala	Thr	Leu	Ile	Thr	Val	Met	Leu	Ala	Phe	Ile	Met	Tyr	Met
				350					355					360
Thr	Leu	Arg	Asn	Ala	Thr	Gln	Gln	Lys	Asp	Met	Val	Glu	Asn	Pro
				365					370					375
Glu	Pro	Pro	Ser	Gly	Val	Arg	Cys	Cys	Cys	Gln	Met	Cys	Cys	Gly
				380					385					390
Pro	Phe	Leu	Leu	Glu	Thr	Pro	Ser	Glu	Tyr	Leu	Glu	Ile	Val	Arg
				395					400					405
Glu	Asn	His	Gly	Leu	Leu	Pro	Pro	Leu	Tyr	Lys	Ser	Val	Lys	Thr
				410					415					420

Tyr Thr Val

<210> 242
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 242
 catttcctta ccctggaccc agctcc 26

<210> 243
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
gaaaggccca cagcacatct ggcag 25

<210> 244
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 244
ccacgaccg agcaacttcc tcaagaccga cttgtttctc tacagc 46

<210> 245
<211> 485
<212> DNA
<213> Homo sapiens

<400> 245
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50
gctcccagat ctggggccgct tgctctctgc tcctcctcct cctcgccagc 100
ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150
gcaaccccag gacagagctg gagccagggc cagctggatg cccatgttcc 200
agaggcgaag gagggcgagac acccacttcc ccattctgcat tttctgctgc 250
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300
acctgccctg ccccgctccc ctcccttctt tatttattcc tgctgcccc 350
gaacataggt cttggaataa aatggctggt tcttttgttt tccaaaaaaaa 400
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485

<210> 246
<211> 84
<212> PRT
<213> Homo sapiens

<400> 246
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu 15
1 5 10
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln 30
20 25 30
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala 45
35 40 45
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp 60
50 55 60
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg 75
65 70 75

Ser Lys Cys Gly Met Cys Cys Lys Thr
80

<210> 247
<211> 2359
<212> DNA
<213> Homo sapiens

<400> 247
ctgtcaggaa ggaccatctg aaggctgcaa tttgttctta gggaggcagg 50
tgctggcctg gcttggatct tccaccatgt tctgttgct gccttttgat 100
agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcaccct 150
ccttctcggtt ttcacatag tgccagccat ttttgagtc tcctttggta 200
tccgcaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250
ttgagaatgg agcaggaggc caaggagaag aaccaccagc tttacaagcc 300
ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350
tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caacactcca 400
gagttcgagc tctctgacat tttctacttt tgccggaaaag gaatggagac 450
cattatggat gatgagggtga caaagagatt ctgagcagaa gaactggagt 500
cctggaacct gctgagcaga accaattata acttcagta catcagcctt 550
cggctcacgg tctgtgggg gttaggagtg ctgattcggg actgctttct 600
gctgccgctc aggatagcac tggctttcac agggattagc cttctggtgg 650
tgggcacaac tgtggtggga tacttgccaa atgggagggt taaggaattc 700
atgagtaaac atgttcactt aatgtgttac cggatctgcg tgcgagcgct 750
gacagccatc atcacctacc atgacaggga aaacagacca agaaatggtg 800
gcatctgtgt ggccaatcat acctaccga tcgatgtgat catcttggcc 850
agcgatggct attatgcat ggtgggtcaa gtgcacgggg gactcatggg 900
tgtgattcag agagccatgg tgaaggcctg cccacacgtc tggtttgagc 950
gctcggaagt gaaggatcg cactggtgg ctaagagact gactgaacat 1000
gtgcaagata aaagcaagct gcctatcctc atcttcccag aaggaacctg 1050
catcaataat acatcggtga tgatgttcaa aaagggaagt tttgaaattg 1100
gagccacagt ttaccctgtt gctatcaagt atgacctca atttggcgat 1150
gccttctgga acagcagcaa atacgggatg gtgacgtacc tgctgcgaat 1200
gatgaccagc tgggccattg tctgcagcgt gtggtacctg cctcccatga 1250
ctagagaggc agatgaagat gctgtccagt ttgcgaatag ggtgaaatct 1300
gccattgccca ggcagggagg acttgtggac ctgctgtggg atgggggcct 1350

gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400
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cggcctcaac atcgccccca gccttgagc tctgcagaca tgataggaag 1950
gaaactgtca tctgcagggg ctttcagcaa aatgaagggt tagattttta 2000
tgctgctgct gatgggggta ctaaaggag ggaagaggc cagggtgggc 2050
gctgactggg ccatggggag aacgtgtgtt cgtactccag gctaaccctg 2100
aactccccat gtgatgcgcg ctttggtgaa tgtgtgtctc ggtttcccc 2150
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gttggtgggga ttaaagtgtc gcgggtgagt gaaggacaca tcacgttcag 2250
tgtttcaagt acaggccac aaaacggggc acggcaggcc tgagctcaga 2300
gctgctgcac tgggctttgg atttgttcct gtgagtaaata aaaactggct 2350
ggtgaatga 2359

<210> 248
<211> 456
<212> PRT
<213> Homo sapiens

<400> 248
Met Phe Leu Leu Leu Pro Phe Asp Ser Leu Ile Val Asn Leu Leu
1 5 10 15
Gly Ile Ser Leu Thr Val Leu Phe Thr Leu Leu Leu Val Phe Ile
20 25 30
Ile Val Pro Ala Ile Phe Gly Val Ser Phe Gly Ile Arg Lys Leu
35 40 45
Tyr Met Lys Ser Leu Leu Lys Ile Phe Ala Trp Ala Thr Leu Arg
50 55 60
Met Glu Arg Gly Ala Lys Glu Lys Asn His Gln Leu Tyr Lys Pro
65 70 75

Tyr	Thr	Asn	Gly	Ile	Ile	Ala	Lys	Asp	Pro	Thr	Ser	Leu	Glu	Glu	
				80					85					90	
Glu	Ile	Lys	Glu	Ile	Arg	Arg	Ser	Gly	Ser	Ser	Lys	Ala	Leu	Asp	
				95					100					105	
Asn	Thr	Pro	Glu	Phe	Glu	Leu	Ser	Asp	Ile	Phe	Tyr	Phe	Cys	Arg	
				110					115					120	
Lys	Gly	Met	Glu	Thr	Ile	Met	Asp	Asp	Glu	Val	Thr	Lys	Arg	Phe	
				125					130					135	
Ser	Ala	Glu	Glu	Leu	Glu	Ser	Trp	Asn	Leu	Leu	Ser	Arg	Thr	Asn	
				140					145					150	
Tyr	Asn	Phe	Gln	Tyr	Ile	Ser	Leu	Arg	Leu	Thr	Val	Leu	Trp	Gly	
				155					160					165	
Leu	Gly	Val	Leu	Ile	Arg	Tyr	Cys	Phe	Leu	Leu	Pro	Leu	Arg	Ile	
				170					175					180	
Ala	Leu	Ala	Phe	Thr	Gly	Ile	Ser	Leu	Leu	Val	Val	Gly	Thr	Thr	
				185					190					195	
Val	Val	Gly	Tyr	Leu	Pro	Asn	Gly	Arg	Phe	Lys	Glu	Phe	Met	Ser	
				200					205					210	
Lys	His	Val	His	Leu	Met	Cys	Tyr	Arg	Ile	Cys	Val	Arg	Ala	Leu	
				215					220					225	
Thr	Ala	Ile	Ile	Thr	Tyr	His	Asp	Arg	Glu	Asn	Arg	Pro	Arg	Asn	
				230					235					240	
Gly	Gly	Ile	Cys	Val	Ala	Asn	His	Thr	Ser	Pro	Ile	Asp	Val	Ile	
				245					250					255	
Ile	Leu	Ala	Ser	Asp	Gly	Tyr	Tyr	Ala	Met	Val	Gly	Gln	Val	His	
				260					265					270	
Gly	Gly	Leu	Met	Gly	Val	Ile	Gln	Arg	Ala	Met	Val	Lys	Ala	Cys	
				275					280					285	
Pro	His	Val	Trp	Phe	Glu	Arg	Ser	Glu	Val	Lys	Asp	Arg	His	Leu	
				290					295					300	
Val	Ala	Lys	Arg	Leu	Thr	Glu	His	Val	Gln	Asp	Lys	Ser	Lys	Leu	
				305					310					315	
Pro	Ile	Leu	Ile	Phe	Pro	Glu	Gly	Thr	Cys	Ile	Asn	Asn	Thr	Ser	
				320					325					330	
Val	Met	Met	Phe	Lys	Lys	Gly	Ser	Phe	Glu	Ile	Gly	Ala	Thr	Val	
				335					340					345	
Tyr	Pro	Val	Ala	Ile	Lys	Tyr	Asp	Pro	Gln	Phe	Gly	Asp	Ala	Phe	
				350					355					360	
Trp	Asn	Ser	Ser	Lys	Tyr	Gly	Met	Val	Thr	Tyr	Leu	Leu	Arg	Met	
				365					370					375	
Met	Thr	Ser	Trp	Ala	Ile	Val	Cys	Ser	Val	Trp	Tyr	Leu	Pro	Pro	
				380					385					390	

Met	Thr	Arg	Glu	Ala	Asp	Glu	Asp	Ala	Val	Gln	Phe	Ala	Asn	Arg
				395					400				405	
Val	Lys	Ser	Ala	Ile	Ala	Arg	Gln	Gly	Gly	Leu	Val	Asp	Leu	Leu
				410					415				420	
Trp	Asp	Gly	Gly	Leu	Lys	Arg	Glu	Lys	Val	Lys	Asp	Thr	Phe	Lys
				425					430					435
Glu	Glu	Gln	Gln	Lys	Leu	Tyr	Ser	Lys	Met	Ile	Val	Gly	Asn	His
				440					445					450
Lys	Asp	Arg	Ser	Arg	Ser									
				455										

<210> 249
 <211> 1103
 <212> DNA
 <213> Homo sapiens

<400> 249
 gccctcgaa accaggactc cagcacctct ggtcccggcc tcacccggac 50
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 gccctcggca gcctcggcct ccacacctgg caggcccagg ctgttccac 150
 catcctgccc ctgggcctgg ctccagacac ctttgacgat acctatgtgg 200
 gttgtgcaga ggagatggag gagaaggcag cccccctgct aaaggaggaa 250
 atggcccacc atgccctgct gcgggaatcc tgggaggcag cccaggagac 300
 ctgggaggac aagcgtcgag ggcttacctt gccccctggc ttcaaagccc 350
 agaatggaat agccattatg gtctacacca actcatcgaa caccttgtac 400
 tgggagttga atcaggccgt gcggacgggc ggaggctccc gggagctcta 450
 catgaggcac tttcccttca aggccctgca tttctacctg atccggggccc 500
 tgcagctgct gcgaggcagt gggggctgca gcaggggacc tggggagggtg 550
 gtgttccgag gtgtgggcag ccttcgcttt gaacccaaga ggctggggga 600
 ctctgtccgc ttgggccagt ttgcctccag ctccctggat aaggcagtgg 650
 cccacagatt tggggagaag aggcggggct gtgtgtctgc gccaggggtg 700
 cagctagggt cacaatctga gggggcctcc tctctgcccc cctggaagac 750
 tctgctcttg gcccctggag agttccagct ctcaggggtt gggccctgaa 800
 agtccaacat ctgccactta ggagccctgg gaacgggtga ccttcatatg 850
 acgaagaggc acctccagca gccttgagaa gcaagaacat ggttccggac 900
 ccagccctag cagccttctc cccaaccagg atgttggcct ggggaggcca 950
 cagcagggtg gagggaaact tgctatgtga tggggacttc ctgggacaag 1000
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gacatggagt tttattgagg tagctacgtg attaaatggt attgcagtgt 1100

gga 1103

<210> 250

<211> 240

<212> PRT

<213> Homo sapiens

<400> 250

Met Ala Leu Ala Ala Leu Met Ile Ala Leu Gly Ser Leu Gly Leu
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His Thr Trp Gln Ala Gln Ala Val Pro Thr Ile Leu Pro Leu Gly
20 25 30

Leu Ala Pro Asp Thr Phe Asp Asp Thr Tyr Val Gly Cys Ala Glu
35 40 45

Glu Met Glu Glu Lys Ala Ala Pro Leu Leu Lys Glu Glu Met Ala
50 55 60

His His Ala Leu Leu Arg Glu Ser Trp Glu Ala Ala Gln Glu Thr
65 70 75

Trp Glu Asp Lys Arg Arg Gly Leu Thr Leu Pro Pro Gly Phe Lys
80 85 90

Ala Gln Asn Gly Ile Ala Ile Met Val Tyr Thr Asn Ser Ser Asn
95 100 105

Thr Leu Tyr Trp Glu Leu Asn Gln Ala Val Arg Thr Gly Gly Gly
110 115 120

Ser Arg Glu Leu Tyr Met Arg His Phe Pro Phe Lys Ala Leu His
125 130 135

Phe Tyr Leu Ile Arg Ala Leu Gln Leu Leu Arg Gly Ser Gly Gly
140 145 150

Cys Ser Arg Gly Pro Gly Glu Val Val Phe Arg Gly Val Gly Ser
155 160 165

Leu Arg Phe Glu Pro Lys Arg Leu Gly Asp Ser Val Arg Leu Gly
170 175 180

Gln Phe Ala Ser Ser Ser Leu Asp Lys Ala Val Ala His Arg Phe
185 190 195

Gly Glu Lys Arg Arg Gly Cys Val Ser Ala Pro Gly Val Gln Leu
200 205 210

Gly Ser Gln Ser Glu Gly Ala Ser Ser Leu Pro Pro Trp Lys Thr
215 220 225

Leu Leu Leu Ala Pro Gly Glu Phe Gln Leu Ser Gly Val Gly Pro
230 235 240

<210> 251

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

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<210> 252

<211> 1076

<212> DNA

<213> Homo sapiens

<400> 252

gtggcttcat ttcagtggct gacttccaga gagcaatatg gctgggtccc 50

caacatgcct caccctcatc tatatccttt ggcagctcac agggtcagca 100

gcctctggac ccgtgaaaga gctggtcggg tccgttgggtg gggccgtgac 150

tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200

tcaacacaac ccctcttgct accatacagc cagaaggggg cactatcata 250

gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta 300

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tggggatata cagctcatca ctccagcagc cctccacca ggagtacgtg 400

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aatgagtccc ataatgggtc catcctcccc atctcctgga gatggggaga 600

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cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac 800

aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact 850

cctaacatat gccccattc tggagagaac acagagtacg acacaatccc 900

tcacactaat agaacaatcc taaaggaaga tccagcaaact acggtttact 950

ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcagc 1000

atgccagaca caccaaggct atttgcctat gagaatgtta tctagacagc 1050

agtgcactcc cctaagtctc tgctca 1076

<210> 253

<211> 335

<212> PRT

<213> Homo sapiens

<400> 253

Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp

1	5	10	15
Gln Leu Thr Gly	Ser Ala Ala Ser Gly	Pro Val Lys Glu Leu Val	
	20	25	30
Gly Ser Val Gly	Gly Ala Val Thr Phe	Pro Leu Lys Ser Lys Val	
	35	40	45
Lys Gln Val Asp	Ser Ile Val Trp Thr	Phe Asn Thr Thr Pro Leu	
	50	55	60
Val Thr Ile Gln	Pro Glu Gly Gly Thr	Ile Ile Val Thr Gln Asn	
	65	70	75
Arg Asn Arg Glu	Arg Val Asp Phe Pro	Asp Gly Gly Tyr Ser Leu	
	80	85	90
Lys Leu Ser Lys	Leu Lys Lys Asn Asp	Ser Gly Ile Tyr Tyr Val	
	95	100	105
Gly Ile Tyr Ser	Ser Ser Leu Gln Gln	Pro Ser Thr Gln Glu Tyr	
	110	115	120
Val Leu His Val	Tyr Glu His Leu Ser	Lys Pro Lys Val Thr Met	
	125	130	135
Gly Leu Gln Ser	Asn Lys Asn Gly Thr	Cys Val Thr Asn Leu Thr	
	140	145	150
Cys Cys Met Glu	His Gly Glu Glu Asp	Val Ile Tyr Thr Trp Lys	
	155	160	165
Ala Leu Gly Gln	Ala Ala Asn Glu Ser	His Asn Gly Ser Ile Leu	
	170	175	180
Pro Ile Ser Trp	Arg Trp Gly Glu Ser	Asp Met Thr Phe Ile Cys	
	185	190	195
Val Ala Arg Asn	Pro Val Ser Arg Asn	Phe Ser Ser Pro Ile Leu	
	200	205	210
Ala Arg Lys Leu	Cys Glu Gly Ala Ala	Asp Asp Pro Asp Ser Ser	
	215	220	225
Met Val Leu Leu	Cys Leu Leu Leu Val	Pro Leu Leu Leu Ser Leu	
	230	235	240
Phe Val Leu Gly	Leu Phe Leu Trp Phe	Leu Lys Arg Glu Arg Gln	
	245	250	255
Glu Glu Tyr Ile	Glu Glu Lys Lys Arg	Val Asp Ile Cys Arg Glu	
	260	265	270
Thr Pro Asn Ile	Cys Pro His Ser Gly	Glu Asn Thr Glu Tyr Asp	
	275	280	285
Thr Ile Pro His	Thr Asn Arg Thr Ile	Leu Lys Glu Asp Pro Ala	
	290	295	300
Asn Thr Val Tyr	Ser Thr Val Glu Ile	Pro Lys Lys Met Glu Asn	
	305	310	315
Pro His Ser Leu	Leu Thr Met Pro Asp	Thr Pro Arg Leu Phe Ala	

Tyr Glu Asn Val Ile
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<210> 254
<211> 1053
<212> DNA
<213> Homo sapiens

<400> 254
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ggccgtgact ttccccctga agtccaaagt aaagcaagtt gactctattg 150
tctggacctt caacacaacc cctcttgtca ccatacagcc agaagggggc 200
actatcatag tgacccaaaa tcgtaatagg gagagagtag acttcccaga 250
tggaggctac tccctgaagc tcagcaaact gaagaagaat gactcagggg 300
tctactatgt ggggatatac agctcatcac tccagcagcc ctccaccag 350
gagtacgtgc tgcattgtta cgagcacctg tcaaagccta aagtcacat 400
gggtctgcag agcaataaga atggcacctg tgtgaccaat ctgacatgct 450
gcatggaaca tggggaagag gatgtgattt atacctggaa ggccctgggg 500
caagcagcca atgagtccca taatgggtcc atcctcccca tctcctggag 550
atggggagaa agtgatatga ccttcatctg cgttgccagg aaccctgtca 600
gcagaaaactt ctcaagcccc atccttgcca ggaagctctg tgaagggtgct 650
gctgatgacc cagattcctc catggtcctc ctgtgtctcc tgttggtgcc 700
cctcctgctc agtctctttg tactgggggt atttcttttg tttctgaaga 750
gagagagaca agaagagtac attgaagaga agaagagagt ggacatttgt 800
cgggaaactc ctaacatatg cccccattct ggagagaaca cagagtacga 850
cacaatccct cacactaata gaacaatcct aaaggaagat ccagcaaata 900
cggtttactc cactgtggaa ataccgaaaa agatggaaaa tccccactca 950
ctgctcacga tgccagacac accaaggcta tttgcctatg agaatgttat 1000
ctagacagca gtgcactccc ctaagtctct gctcaaaaaa aaaaaaaaaa 1050
aaa 1053

<210> 255
<211> 860
<212> DNA
<213> Homo sapiens

<400> 255
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 aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150
 gaatggcata ctattatcct ggcctctgac aaaagagaaa agatagaaga 200
 acatggcaac tttagacttt ttctggagca aatccatgtc ttggagaatt 250
 ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300
 tctatgggtg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350
 tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400
 ttatggctca cctcattaac gaaaaggatg gggaaacctt ccagctgatg 450
 gggctctatg gccgagaacc agatttgagt tcagacatca aggaaagggt 500
 tgcacaacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550
 tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600
 gcctccagtg ttgagtggac acttctcacc aggactccac catcatccct 650
 tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700
 ctgtctcact gagaagtcca attccagtct atcaacatgt tacctaggat 750
 acctcatcaa gaatcaaaga cttcttttaa tttctctttg atacaccctt 800
 gacaattttt catgaaatta ttctcttccc tgttcaataa atgattaccc 850
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<210> 256

<211> 180

<212> PRT

<213> Homo sapiens

<400> 256

Met	Lys	Met	Leu	Leu	Leu	Leu	Cys	Leu	Gly	Leu	Thr	Leu	Val	Cys	1	5	10	15
Val	His	Ala	Glu	Glu	Ala	Ser	Ser	Thr	Gly	Arg	Asn	Phe	Asn	Val	20	25	30	
Glu	Lys	Ile	Asn	Gly	Glu	Trp	His	Thr	Ile	Ile	Leu	Ala	Ser	Asp	35	40	45	
Lys	Arg	Glu	Lys	Ile	Glu	Glu	His	Gly	Asn	Phe	Arg	Leu	Phe	Leu	50	55	60	
Glu	Gln	Ile	His	Val	Leu	Glu	Asn	Ser	Leu	Val	Leu	Lys	Val	His	65	70	75	
Thr	Val	Arg	Asp	Glu	Glu	Cys	Ser	Glu	Leu	Ser	Met	Val	Ala	Asp	80	85	90	
Lys	Thr	Glu	Lys	Ala	Gly	Glu	Tyr	Ser	Val	Thr	Tyr	Asp	Gly	Phe	95	100	105	
Asn	Thr	Phe	Thr	Ile	Pro	Lys	Thr	Asp	Tyr	Asp	Asn	Phe	Leu	Met	110	115	120	

Ala	His	Leu	Ile	Asn	Glu	Lys	Asp	Gly	Glu	Thr	Phe	Gln	Leu	Met
				125					130					135
Gly	Leu	Tyr	Gly	Arg	Glu	Pro	Asp	Leu	Ser	Ser	Asp	Ile	Lys	Glu
				140					145					150
Arg	Phe	Ala	Gln	Leu	Cys	Glu	Glu	His	Gly	Ile	Leu	Arg	Glu	Asn
				155					160					165
Ile	Ile	Asp	Leu	Ser	Asn	Ala	Asn	Arg	Cys	Leu	Gln	Ala	Arg	Glu
				170					175					180

<210> 257

<211> 766

<212> DNA

<213> Homo sapiens

<400> 257

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ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaatth 150
tctcaaaacc ccatctcttg ctttgagtgg tggttcccag gaattatagg 200
agcaggctctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250
aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300
agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca 350
ggctctctta aaaggctctc tcatgtgtaa ttctccaagc aacagtaatg 400
ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450
ttcaacttgc agtgggtttt caatgactct tgtgcacctc ctactggttt 500
caataaacc accagtaacg acaccatggc gagtggctgg agagcatcta 550
gtttccactt cgattctgaa gaaaacaaac ataggcttat ccactttctca 600
gtatttttag gtctattgct tggttgaatt ctggagggtcc tgtttgggct 650
cagtcagata gtcacggtt tccttggtctg totgtgtgga gtctctaagc 700
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gtttgaaaaa aaaaaa 766

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<210> 258

<211> 229

<212> PRT

<213> Homo sapiens

<400> 258

Met	Thr	Cys	Cys	Glu	Gly	Trp	Thr	Ser	Cys	Asn	Gly	Phe	Ser	Leu
1				5					10					15
Leu	Val	Leu	Leu	Leu	Leu	Gly	Val	Val	Leu	Asn	Ala	Ile	Pro	Leu
				20					25					30
Ile	Val	Ser	Leu	Val	Glu	Glu	Asp	Gln	Phe	Ser	Gln	Asn	Pro	Ile

	35	40	45
Ser Cys Phe Glu Trp Trp Phe Pro Gly Ile Ile Gly Ala Gly Leu	50	55	60
Met Ala Ile Pro Ala Thr Thr Met Ser Leu Thr Ala Arg Lys Arg	65	70	75
Ala Cys Cys Asn Asn Arg Thr Gly Met Phe Leu Ser Ser Phe Phe	80	85	90
Ser Val Ile Thr Val Ile Gly Ala Leu Tyr Cys Met Leu Ile Ser	95	100	105
Ile Gln Ala Leu Leu Lys Gly Pro Leu Met Cys Asn Ser Pro Ser	110	115	120
Asn Ser Asn Ala Asn Cys Glu Phe Ser Leu Lys Asn Ile Ser Asp	125	130	135
Ile His Pro Glu Ser Phe Asn Leu Gln Trp Phe Phe Asn Asp Ser	140	145	150
Cys Ala Pro Pro Thr Gly Phe Asn Lys Pro Thr Ser Asn Asp Thr	155	160	165
Met Ala Ser Gly Trp Arg Ala Ser Ser Phe His Phe Asp Ser Glu	170	175	180
Glu Asn Lys His Arg Leu Ile His Phe Ser Val Phe Leu Gly Leu	185	190	195
Leu Leu Val Gly Ile Leu Glu Val Leu Phe Gly Leu Ser Gln Ile	200	205	210
Val Ile Gly Phe Leu Gly Cys Leu Cys Gly Val Ser Lys Arg Arg	215	220	225
Ser Gln Ile Val			

<210> 259
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 259
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 gctaccaggc ccatgctctt gtctgccag ctgttgcttc tgagatcaca 150
 gtcttcttat tcttaagtga cgctgcggtta aacctccaag ttgccaaaact 200
 taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250
 ccgatcagat atcttttaag aaacgactct cattgaaaaa gtcttggtgg 300
 aaatagttaa aaaatgtggt gtgtgacatg taaaaatgct caacctggtt 350
 tccaaagtct ttcaacgaca cctgatctt cactaaaaat tgtaaagggt 400

tcaacacgtt gctttaataa atcacttgcc ctgc 434

<210> 260

<211> 83

<212> PRT

<213> Homo sapiens

<400> 260

Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys
1 5 10 15

Cys Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu
20 25 30

Ile Thr Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln
35 40 45

Val Ala Lys Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu
50 55 60

Glu Val Lys His Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu
65 70 75

Ser Leu Lys Lys Ser Trp Trp Lys
80

<210> 261

<211> 636

<212> DNA

<213> Homo sapiens

<400> 261

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ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150

cgccccagtg cctctcccc tgcagccctg cccctcgaac tgtgacatgg 200

agagagtgac cctggccctt ctctactgg caggcctgac tgccttggaa 250

gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300

aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg 350

ggatcgcggc agttctgagt ggcaaatgca aatacaagag cagccagaag 400

cagcacagtc ctgtacctga gaaggccatc ccaactcatca ctccaggctc 450

tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc 500

taacactggc ccccagcacc tcctcccctg ggaggcctta tcctcaagga 550

aggacttctc tccaagggca ggctgttagg cccctttctg atcaggaggc 600

ttctttatga attaaactcg cccaccacc ccctca 636

<210> 262

<211> 89

<212> PRT

<213> Homo sapiens

<400> 262

Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr
1 5 10 15

Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe
20 25 30

Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly
35 40 45

Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys
50 55 60

Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu
65 70 75

Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys
80 85

<210> 263

<211> 1676

<212> DNA

<213> Homo sapiens

<400> 263

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actcctgctg ctggttgtgg gctcctgggt actcgccgc atcctggctt 150

ggacctatgc cttctataac aactgccgcc ggctccagtg tttcccacag 200

ccccaaaac ggaactggtt ttgggggtcac ctgggcctga tcactcctac 250

agaggagggc ttgaaggact cgaccagat gtcggccacc tattcccagg 300

gctttacggt atggctgggt cccatcatcc ccttcacgt tttatgccac 350

cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcacccaa 400

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tgctgagtgg cggtgacaag tggagccgcc accgtcggat gctgacgccc 500

gccttccatt tcaacatcct gaagtcctat ataacgatct tcaacaagag 550

tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca 600

gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta 650

cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga 700

atatattgcc accatcttgg agctcagtgc ccttgtagag aaaagaagcc 750

agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg 800

cggcgcttcc acagggcctg ccgcctgggtg catgacttca cagacgctgt 850

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<210> 264

<211> 524

<212> PRT

<213> Homo sapiens

<400> 264

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Met	Ser	Pro	Trp	Leu	Leu	Leu	Leu	Leu	Val	Val	Gly	Ser	Trp	Leu
				20					25					30
Leu	Ala	Arg	Ile	Leu	Ala	Trp	Thr	Tyr	Ala	Phe	Tyr	Asn	Asn	Cys
				35					40					45
Arg	Arg	Leu	Gln	Cys	Phe	Pro	Gln	Pro	Pro	Lys	Arg	Asn	Trp	Phe
				50					55					60
Trp	Gly	His	Leu	Gly	Leu	Ile	Thr	Pro	Thr	Glu	Glu	Gly	Leu	Lys
				65					70					75
Asp	Ser	Thr	Gln	Met	Ser	Ala	Thr	Tyr	Ser	Gln	Gly	Phe	Thr	Val
				80					85					90
Trp	Leu	Gly	Pro	Ile	Ile	Pro	Phe	Ile	Val	Leu	Cys	His	Pro	Asp
				95					100					105
Thr	Ile	Arg	Ser	Ile	Thr	Asn	Ala	Ser	Ala	Ala	Ile	Ala	Pro	Lys
				110					115					120
Asp	Asn	Leu	Phe	Ile	Arg	Phe	Leu	Lys	Pro	Trp	Leu	Gly	Glu	Gly
				125					130					135

Ile	Leu	Leu	Ser	Gly	Gly	Asp	Lys	Trp	Ser	Arg	His	Arg	Arg	Met
				140					145					150
Leu	Thr	Pro	Ala	Phe	His	Phe	Asn	Ile	Leu	Lys	Ser	Tyr	Ile	Thr
				155					160					165
Ile	Phe	Asn	Lys	Ser	Ala	Asn	Ile	Met	Leu	Asp	Lys	Trp	Gln	His
				170					175					180
Leu	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Leu	Asp	Met	Phe	Glu	His	Ile
				185					190					195
Ser	Leu	Met	Thr	Leu	Asp	Ser	Leu	Gln	Lys	Cys	Ile	Phe	Ser	Phe
				200					205					210
Asp	Ser	His	Cys	Gln	Glu	Arg	Pro	Ser	Glu	Tyr	Ile	Ala	Thr	Ile
				215					220					225
Leu	Glu	Leu	Ser	Ala	Leu	Val	Glu	Lys	Arg	Ser	Gln	His	Ile	Leu
				230					235					240
Gln	His	Met	Asp	Phe	Leu	Tyr	Tyr	Leu	Ser	His	Asp	Gly	Arg	Arg
				245					250					255
Phe	His	Arg	Ala	Cys	Arg	Leu	Val	His	Asp	Phe	Thr	Asp	Ala	Val
				260					265					270
Ile	Arg	Glu	Arg	Arg	Arg	Thr	Leu	Pro	Thr	Gln	Gly	Ile	Asp	Asp
				275					280					285
Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp
				290					295					300
Val	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp
				305					310					315
Glu	Asp	Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	His
				320					325					330
Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	Leu	Ala
				335					340					345
Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	Glu
				350					355					360
Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu
				365					370					375
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg
				380					385					390
Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp
				395					400					405
Ile	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys
				410					415					420
Leu	Ile	Asp	Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro
				425					430					435
Asp	Pro	Glu	Val	Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser
				440					445					450

Lys	Gly	Arg	Ser	Pro	Leu	Ala	Phe	Ile	Pro	Phe	Ser	Ala	Gly	Pro	455	460	465
Arg	Asn	Cys	Ile	Gly	Gln	Ala	Phe	Ala	Met	Ala	Glu	Met	Lys	Val	470	475	480
Val	Leu	Ala	Leu	Met	Leu	Leu	His	Phe	Arg	Phe	Leu	Pro	Asp	His	485	490	495
Thr	Glu	Pro	Arg	Arg	Lys	Leu	Glu	Leu	Ile	Met	Arg	Ala	Glu	Gly	500	505	510
Gly	Leu	Trp	Leu	Arg	Val	Glu	Pro	Leu	Asn	Val	Gly	Leu	Gln		515	520	

<210> 265
 <211> 584
 <212> DNA
 <213> Homo sapiens

<400> 265
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 gccagaatct ggaaaccata caagaaacgt gagactcctg attgcttctg 400
 gaaataactgt gtctgaagtg aaataagcat ctgttagtca gctcagaaac 450
 acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500
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 aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 266
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 Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser
 20 25 30
 Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu
 35 40 45
 Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu
 50 55 60

Gly Ala Glu Arg Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr
65 70 75
Asn Ile Phe Asn Pro Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe
80 85 90
Ser Gly Gln Asp Pro Asn Ile Leu Leu Ser His Leu Leu Ala Arg
95 100 105
Ile Trp Lys Pro Tyr Lys Lys Arg Glu Thr Pro Asp Cys Phe Trp
110 115 120
Lys Tyr Cys Val

<210> 267
<211> 654
<212> DNA
<213> Homo sapiens

<400> 267
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<210> 268
<211> 117
<212> PRT
<213> Homo sapiens

<400> 268
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Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro
20 25 30
Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro
35 40 45

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<210> 272

<211> 285

<212> PRT

<213> Homo sapiens

<400> 272

Met	Ala	Lys	Met	Glu	Leu	Ser	Lys	Ala	Phe	Ser	Gly	Gln	Arg	Thr
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Leu	Leu	Ser	Ala	Ile	Leu	Ser	Met	Leu	Ser	Leu	Ser	Phe	Ser	Thr
				20					25					30

Thr	Ser	Leu	Leu	Ser	Asn	Tyr	Trp	Phe	Val	Gly	Thr	Gln	Lys	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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<210> 274

<211> 86

<212> PRT

<213> Homo sapiens

<400> 274

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Pro	Ile	Leu	Ser	Ser	Pro	Ser	Leu	Lys	Ser	Gln	Ala	Cys	Gln	Gln
				20					25					30
Leu	Leu	Trp	Thr	Leu	Pro	Ser	Pro	Leu	Val	Ala	Phe	Arg	Ala	Asn
				35					40					45
Arg	Thr	Thr	Tyr	Val	Met	Asp	Val	Ser	Thr	Asn	Gln	Gly	Ser	Gly
				50					55					60
Met	Glu	His	Arg	Asn	His	Leu	Cys	Phe	Cys	Asp	Leu	Tyr	Asp	Arg
				65					70					75
Ala	Thr	Ser	Pro	Pro	Leu	Lys	Cys	Ser	Leu	Leu				
				80					85					

35

40

45

Pro Ile Pro Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp
50 55 60

Ala Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr
65 70 75

Gly Ile Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg
80 85 90

Ala His Leu Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly
95 100 105

Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe
110 115 120

Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln Trp
125 130

<210> 277

<211> 4104

<212> DNA

<213> Homo sapiens

<400> 277

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<210> 278
 <211> 522
 <212> PRT
 <213> Homo sapiens

<400> 278

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Arg	Pro	Ser	Gly	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala	Cys	Phe	Gln	20	25	30	
Met	Leu	Pro	Ala	Ala	Pro	Ser	Gly	Cys	Pro	Gln	Leu	Cys	Arg	Cys	35	40	45	
Glu	Gly	Arg	Leu	Leu	Tyr	Cys	Glu	Ala	Leu	Asn	Leu	Thr	Glu	Ala	50	55	60	
Pro	His	Asn	Leu	Ser	Gly	Leu	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	65	70	75	
Ser	Leu	Ser	Glu	Leu	Arg	Ala	Gly	Gln	Phe	Thr	Gly	Leu	Met	Gln	80	85	90	
Leu	Thr	Trp	Leu	Tyr	Leu	Asp	His	Asn	His	Ile	Cys	Ser	Val	Gln	95	100	105	
Gly	Asp	Ala	Phe	Gln	Lys	Leu	Arg	Arg	Val	Lys	Glu	Leu	Thr	Leu	110	115	120	
Ser	Ser	Asn	Gln	Ile	Thr	Gln	Leu	Pro	Asn	Thr	Thr	Phe	Arg	Pro	125	130	135	
Met	Pro	Asn	Leu	Arg	Ser	Val	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Gln	140	145	150	
Ala	Leu	Ala	Pro	Asp	Leu	Phe	His	Gly	Leu	Arg	Lys	Leu	Thr	Thr	155	160	165	
Leu	His	Met	Arg	Ala	Asn	Ala	Ile	Gln	Phe	Val	Pro	Val	Arg	Ile	170	175	180	
Phe	Gln	Asp	Cys	Arg	Ser	Leu	Lys	Phe	Leu	Asp	Ile	Gly	Tyr	Asn	185	190	195	
Gln	Leu	Lys	Ser	Leu	Ala	Arg	Asn	Ser	Phe	Ala	Gly	Leu	Phe	Lys	200	205	210	
Leu	Thr	Glu	Leu	His	Leu	Glu	His	Asn	Asp	Leu	Val	Lys	Val	Asn	215	220	225	
Phe	Ala	His	Phe	Pro	Arg	Leu	Ile	Ser	Leu	His	Ser	Leu	Cys	Leu	230	235	240	
Arg	Arg	Asn	Lys	Val	Ala	Ile	Val	Val	Ser	Ser	Leu	Asp	Trp	Val	245	250	255	
Trp	Asn	Leu	Glu	Lys	Met	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Tyr	260	265	270	
Met	Glu	Pro	His	Val	Phe	Glu	Thr	Val	Pro	His	Leu	Gln	Ser	Leu	275	280	285	

Gln	Leu	Asp	Ser	Asn	Arg	Leu	Thr	Tyr	Ile	Glu	Pro	Arg	Ile	Leu	290	295	300
Asn	Ser	Trp	Lys	Ser	Leu	Thr	Ser	Ile	Thr	Leu	Ala	Gly	Asn	Leu	305	310	315
Trp	Asp	Cys	Gly	Arg	Asn	Val	Cys	Ala	Leu	Ala	Ser	Trp	Leu	Ser	320	325	330
Asn	Phe	Gln	Gly	Arg	Tyr	Asp	Gly	Asn	Leu	Gln	Cys	Ala	Ser	Pro	335	340	345
Glu	Tyr	Ala	Gln	Gly	Glu	Asp	Val	Leu	Asp	Ala	Val	Tyr	Ala	Phe	350	355	360
His	Leu	Cys	Glu	Asp	Gly	Ala	Glu	Pro	Thr	Ser	Gly	His	Leu	Leu	365	370	375
Ser	Ala	Val	Thr	Asn	Arg	Ser	Asp	Leu	Gly	Pro	Pro	Ala	Ser	Ser	380	385	390
Ala	Thr	Thr	Leu	Ala	Asp	Gly	Gly	Glu	Gly	Gln	His	Asp	Gly	Thr	395	400	405
Phe	Glu	Pro	Ala	Thr	Val	Ala	Leu	Pro	Gly	Gly	Glu	His	Ala	Glu	410	415	420
Asn	Ala	Val	Gln	Ile	His	Lys	Val	Val	Thr	Gly	Thr	Met	Ala	Leu	425	430	435
Ile	Phe	Ser	Phe	Leu	Ile	Val	Val	Leu	Val	Leu	Tyr	Val	Ser	Trp	440	445	450
Lys	Cys	Phe	Pro	Ala	Ser	Leu	Arg	Gln	Leu	Arg	Gln	Cys	Phe	Val	455	460	465
Thr	Gln	Arg	Arg	Lys	Gln	Lys	Gln	Lys	Gln	Thr	Met	His	Gln	Met	470	475	480
Ala	Ala	Met	Ser	Ala	Gln	Glu	Tyr	Tyr	Val	Asp	Tyr	Lys	Pro	Asn	485	490	495
His	Ile	Glu	Gly	Ala	Leu	Val	Ile	Ile	Asn	Glu	Tyr	Gly	Ser	Cys	500	505	510
Thr	Cys	His	Gln	Gln	Pro	Ala	Arg	Glu	Cys	Glu	Val				515	520	

<210> 279

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

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<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

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Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe					
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Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys					
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Leu Ala

<210> 284
 <211> 2623
 <212> DNA
 <213> Homo sapiens

<400> 284
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 gagagaaaat tagggggaga aaggacagag agagcaacta ccatccatag 200
 ccagatagat tatcttacac tgaactgac aagtactttg aaaatgactt 250
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<210> 285

<211> 477
 <212> PRT
 <213> Homo sapiens

<400> 285

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				20					25					30	
Leu	Leu	Val	Ser	Phe	Asp	Gly	Phe	Arg	Trp	Asp	Tyr	Leu	Tyr	Lys	
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Val	Pro	Thr	Pro	His	Phe	His	Tyr	Ile	Met	Lys	Tyr	Gly	Val	His	
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Val	Lys	Gln	Val	Thr	Asn	Val	Phe	Ile	Thr	Lys	Thr	Tyr	Pro	Asn	
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His	Tyr	Thr	Leu	Val	Thr	Gly	Leu	Phe	Ala	Glu	Asn	His	Gly	Ile	
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Val	Ala	Asn	Asp	Met	Phe	Asp	Pro	Ile	Arg	Asn	Lys	Ser	Phe	Ser	
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Leu	Asp	His	Met	Asn	Ile	Tyr	Asp	Ser	Lys	Phe	Trp	Glu	Glu	Ala	
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Thr	Pro	Ile	Trp	Ile	Thr	Asn	Gln	Arg	Ala	Gly	His	Thr	Ser	Gly	
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Ala	Ala	Met	Trp	Pro	Gly	Thr	Asp	Val	Lys	Ile	His	Lys	Arg	Phe	
				140					145					150	
Pro	Thr	His	Tyr	Met	Pro	Tyr	Asn	Glu	Ser	Val	Ser	Phe	Glu	Asp	
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Arg	Val	Ala	Lys	Ile	Val	Glu	Trp	Phe	Thr	Ser	Lys	Glu	Pro	Ile	
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Asn	Leu	Gly	Leu	Leu	Tyr	Trp	Glu	Asp	Pro	Asp	Asp	Met	Gly	His	
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				200					205					210	
Ile	Asp	Lys	Lys	Leu	Gly	Tyr	Leu	Ile	Gln	Met	Leu	Lys	Lys	Ala	
				215					220					225	
Lys	Leu	Trp	Asn	Thr	Leu	Asn	Leu	Ile	Ile	Thr	Ser	Asp	His	Gly	
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Met	Thr	Gln	Cys	Ser	Glu	Glu	Arg	Leu	Ile	Glu	Leu	Asp	Gln	Tyr	
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Leu	Asp	Lys	Asp	His	Tyr	Thr	Leu	Ile	Asp	Gln	Ser	Pro	Val	Ala	
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Ser Asp Asp Phe Leu Leu Gly Asn His	Gly Tyr Asp Asn Ala Leu	
335	340	345
Ala Asp Met His Pro Ile Phe Leu Ala	His Gly Pro Ala Phe Arg	
350	355	360
Lys Asn Phe Ser Lys Glu Ala Met Asn	Ser Thr Asp Leu Tyr Pro	
365	370	375
Leu Leu Cys His Leu Leu Asn Ile Thr	Ala Met Pro His Asn Gly	
380	385	390
Ser Phe Trp Asn Val Gln Asp Leu Leu	Asn Ser Ala Met Pro Arg	
395	400	405
Val Val Pro Tyr Thr Gln Ser Thr Ile	Leu Leu Pro Gly Ser Val	
410	415	420
Lys Pro Ala Glu Tyr Asp Gln Glu Gly	Ser Tyr Pro Tyr Phe Ile	
425	430	435
Gly Val Ser Leu Gly Ser Ile Ile Val	Ile Val Phe Phe Val Ile	
440	445	450
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Met	Met	Glu	Ile	Ile	Phe	Lys	Leu	Phe	Val	Phe	Arg	Leu	Ser	Ser	
				155					160					165	
Phe	Thr	Thr	Ser	Leu	Arg	Ser	Trp	Met	Pro	Val	Val	Val	Val	Val	
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Ser	Phe	Ile	Leu	Asp	Ile	Val	Leu	Leu	Phe	Gln	Glu	His	Gln	Phe	
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Glu	Ala	Leu	Gly	Leu	Leu	Ile	Leu	Leu	Arg	Leu	Trp	Arg	Val	Ala	
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Arg	Ile	Ile	Asn	Gly	Ile	Ile	Ile	Ser	Val	Lys	Thr	Arg	Ser	Glu	
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Arg	Gln	Leu	Leu	Arg	Leu	Lys	Gln	Met	Asn	Val	Gln	Leu	Ala	Ala	
				230					235					240	
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<212> DNA

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<211> 469

<212> PRT

<213> Homo sapiens

<400> 289

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			20						25					30

Lys	Ser	Ile	Phe	Lys	Leu	Ser	Val	Phe	Ile	Pro	Ser	Gln	Glu	Phe
			35						40					45

Ser	Thr	Tyr	Arg	Gln	Trp	Lys	Gln	Lys	Ile	Val	Gln	Ala	Gly	Asp
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Lys	Asp	Leu	Asp	Gly	Gln	Leu	Asp	Phe	Glu	Glu	Phe	Val	His	Tyr
			65						70					75

Leu	Gln	Asp	His	Glu	Lys	Lys	Leu	Arg	Leu	Val	Phe	Lys	Ile	Leu
			80						85					90

Asp	Lys	Lys	Asn	Asp	Gly	Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	
				95					100					105	
Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	
				110					115					120	
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp	
				125					130					135	
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn	
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Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp	
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Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe	Thr	Val	Glu	Glu	
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Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala	Gly	Gly	Gly	
				185					190					195	
Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp	Arg	Leu	
				200					205					210	
Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met	Gly	
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Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Arg	
				230					235					240	
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	
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Glu	Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Ile	Lys	Arg	Leu	
				260					265					270	
Val	Gly	Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	
				275					280					285	
Ala	Gly	Ser	Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro	
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Met	Glu	Val	Leu	Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln	
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Tyr	Ser	Gly	Met	Leu	Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Arg	Glu	
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Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly	
				335					340					345	
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu	
				350					355					360	
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro	
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Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys	
				380					385					390	
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met	
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Gln	Ala	Gln	Ala	Ser	Ile	Glu	Gly	Ala	Pro	Glu	Val	Thr	Met	Ser	
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Ser	Leu	Phe	Lys	His	Ile	Leu	Arg	Thr	Glu	Gly	Ala	Phe	Gly	Leu	
				425					430					435	
Tyr	Arg	Gly	Leu	Ala	Pro	Asn	Phe	Met	Lys	Val	Ile	Pro	Ala	Val	
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Ser	Ile	Ser	Tyr	Val	Val	Tyr	Glu	Asn	Leu	Lys	Ile	Thr	Leu	Gly	
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 <213> Homo sapiens

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<212> PRT

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<400> 291

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Asp	Ile	Lys	Leu	Ser	Asp	Ile	Val	Ile	Gln	Trp	Leu	Lys	Glu	Gly	65	70	75	
Val	Leu	Gly	Leu	Val	His	Glu	Phe	Lys	Glu	Gly	Lys	Asp	Glu	Leu	80	85	90	
Ser	Glu	Gln	Asp	Glu	Met	Phe	Arg	Gly	Arg	Thr	Ala	Val	Phe	Ala	95	100	105	
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Gln	Leu	Thr	Asp	Ala	Gly	Thr	Tyr	Lys	Cys	Tyr	Ile	Ile	Thr	Ser	125	130	135	
Lys	Gly	Lys	Gly	Asn	Ala	Asn	Leu	Glu	Tyr	Lys	Thr	Gly	Ala	Phe	140	145	150	
Ser	Met	Pro	Glu	Val	Asn	Val	Asp	Tyr	Asn	Ala	Ser	Ser	Glu	Thr				

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Asn Thr Ser Phe Glu Leu Asn Ser Glu	Asn Val Thr Met Lys Val	
200	205	210
Val Ser Val Leu Tyr Asn Val Thr Ile	Asn Asn Thr Tyr Ser Cys	
215	220	225
Met Ile Glu Asn Asp Ile Ala Lys Ala	Thr Gly Asp Ile Lys Val	
230	235	240
Thr Glu Ser Glu Ile Lys Arg Arg Ser	His Leu Gln Leu Leu Asn	
245	250	255
Ser Lys Ala Ser Leu Cys Val Ser Ser	Phe Phe Ala Ile Ser Trp	
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 ctgcctatta tcccaggagc agttgctggc atgggtgctca ccgtgatagg 700
 aatttcactc tgcatacaca gctcagtgag taagaccagc gggcaacagt 750
 ctaccctttg agtggggcga acccacttcc agctctgctg cctccaggaa 800

Phe	Pro	Leu	Gln	Leu	Phe	Cys	Phe	Leu	Val	Ala	Ile	Arg	Val	Pro
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Phe	Pro	Trp	Thr	Val	Trp	Arg	Lys	Thr	Glu	Ala	Gly	Val	Trp	Asp
				170					175					180

<210> 294
 <211> 1164
 <212> DNA
 <213> Homo sapiens

<400> 294
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 ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctcggt 250
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<210> 295
 <211> 237
 <212> PRT

<213> Homo sapiens

<400> 295

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Ala Val Glu Ser Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys
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Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn
35 40 45

Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro
50 55 60

Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser
65 70 75

Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu
80 85 90

Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys
95 100 105

Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser
110 115 120

Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser
125 130 135

Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val
140 145 150

Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu
155 160 165

Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe
170 175 180

Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
185 190 195

Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro
200 205 210

Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu
215 220 225

Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro
230 235

<210> 296

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 296

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	65		70		75
Arg Leu Ala Gly	Pro Ala Ala Ala Glu	Leu Leu Ala Ala Thr	Val		
	80		85		90
Ser Thr Gly Phe	Ser Arg Ser Ser Ala	Ile Asn Glu Glu Asp	Gly		
	95		100		105
Ser Ser Glu Glu	Gly Val Val Ile Asn	Ala Gly Lys Asp Ser	Thr		
	110		115		120
Ser Arg Glu Leu	Pro Ser Ala Thr Pro	Asn Thr Ala Gly Ser	Ser		
	125		130		135
Ser Thr Arg Phe	Ile Ala Asn Ser Gln	Glu Pro Glu Ile Arg	Leu		
	140		145		150
Thr Ser Ser Leu	Pro Arg Ser Pro Gly	Arg Ser Thr Glu Asp	Leu		
	155		160		165
Pro Gly Ser Gln	Ala Thr Leu Ser Gln	Trp Ser Thr Pro Gly	Ser		
	170		175		180
Thr Pro Ser Arg	Trp Pro Ser Pro Ser	Pro Thr Ala Met Pro	Ser		
	185		190		195
Pro Glu Asp Leu	Arg Leu Val Leu Met	Pro Trp Gly Pro Trp	His		
	200		205		210
Cys His Cys Lys	Ser Gly Thr Met Ser	Arg Ser Arg Ser Gly	Lys		
	215		220		225
Leu His Gly Leu	Ser Gly Arg Leu Arg	Val Gly Ala Leu Ser	Gln		
	230		235		240
Leu Arg Thr Glu	His Lys Pro Cys Thr	Tyr Gln Gln Cys Pro	Cys		
	245		250		255
Asn Arg Leu Arg	Glu Glu Cys Pro Leu	Asp Thr Ser Leu Cys	Thr		
	260		265		270
Asp Thr Asn Cys	Ala Ser Gln Ser Thr	Thr Ser Thr Arg Thr	Thr		
	275		280		285
Thr Thr Pro Phe	Pro Thr Ile His Leu	Arg Ser Ser Pro Ser	Leu		
	290		295		300
Pro Pro Ala Ser	Pro Cys Pro Ala Leu	Ala Phe Trp Lys Arg	Val		
	305		310		315
Arg Ile Gly Leu	Glu Asp Ile Trp Asn	Ser Leu Ser Ser Val	Phe		
	320		325		330
Thr Glu Met Gln	Pro Ile Asp Arg Asn	Gln Arg			
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<210> 298

<211> 2692

<212> DNA

<213> Homo sapiens

<400> 298

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 cgaccgtgag ccggtgtacc gcgactgcgt actgcagtgc gaagagcaga 150
 actgctctgg gggcgctctg aatcacttcc gctcccgccca gccaatctac 200
 atgagtctag caggctggac ctgtcgggac gactgtaagt atgagtgtat 250
 gtgggtcacc gttgggctct acctccagga aggtcacaaa gtgcctcagt 300
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<210> 299

<211> 320

<212> PRT

<213> Homo sapiens

<400> 299

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				20					25					30
Asp	Cys	Val	Leu	Gln	Cys	Glu	Glu	Gln	Asn	Cys	Ser	Gly	Gly	Ala
				35					40					45
Leu	Asn	His	Phe	Arg	Ser	Arg	Gln	Pro	Ile	Tyr	Met	Ser	Leu	Ala
				50					55					60
Gly	Trp	Thr	Cys	Arg	Asp	Asp	Cys	Lys	Tyr	Glu	Cys	Met	Trp	Val
				65					70					75

Thr	Val	Gly	Leu	Tyr	Leu	Gln	Glu	Gly	His	Lys	Val	Pro	Gln	Phe	
				80					85					90	
His	Gly	Lys	Trp	Pro	Phe	Ser	Arg	Phe	Leu	Phe	Phe	Gln	Glu	Pro	
				95					100					105	
Ala	Ser	Ala	Val	Ala	Ser	Phe	Leu	Asn	Gly	Leu	Ala	Ser	Leu	Val	
				110					115					120	
Met	Leu	Cys	Arg	Tyr	Arg	Thr	Phe	Val	Pro	Ala	Ser	Ser	Pro	Met	
				125					130					135	
Tyr	His	Thr	Cys	Val	Ala	Phe	Ala	Trp	Val	Ser	Leu	Asn	Ala	Trp	
				140					145					150	
Phe	Trp	Ser	Thr	Val	Phe	His	Thr	Arg	Asp	Thr	Asp	Leu	Thr	Glu	
				155					160					165	
Lys	Met	Asp	Tyr	Phe	Cys	Ala	Ser	Thr	Val	Ile	Leu	His	Ser	Ile	
				170					175					180	
Tyr	Leu	Cys	Cys	Val	Arg	Thr	Val	Gly	Leu	Gln	His	Pro	Ala	Val	
				185					190					195	
Val	Ser	Ala	Phe	Arg	Ala	Leu	Leu	Leu	Leu	Met	Leu	Thr	Val	His	
				200					205					210	
Val	Ser	Tyr	Leu	Ser	Leu	Ile	Arg	Phe	Asp	Tyr	Gly	Tyr	Asn	Leu	
				215					220					225	
Val	Ala	Asn	Val	Ala	Ile	Gly	Leu	Val	Asn	Val	Val	Trp	Trp	Leu	
				230					235					240	
Ala	Trp	Cys	Leu	Trp	Asn	Gln	Arg	Arg	Leu	Pro	His	Val	Arg	Lys	
				245					250					255	
Cys	Val	Val	Val	Val	Leu	Leu	Leu	Gln	Gly	Leu	Ser	Leu	Leu	Glu	
				260					265					270	
Leu	Leu	Asp	Phe	Pro	Pro	Leu	Phe	Trp	Val	Leu	Asp	Ala	His	Ala	
				275					280					285	
Ile	Trp	His	Ile	Ser	Thr	Ile	Pro	Val	His	Val	Leu	Phe	Phe	Ser	
				290					295					300	
Phe	Leu	Glu	Asp	Asp	Ser	Leu	Tyr	Leu	Leu	Lys	Glu	Ser	Glu	Asp	
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Lys	Phe	Lys	Leu	Asp											
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<210> 300

<211> 1674

<212> DNA

<213> Homo sapiens

<400> 300

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<210> 301

<211> 461
 <212> PRT
 <213> Homo sapiens

<400> 301

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Met	Leu	Leu	Gly	Leu	Leu	Met	Ala	Ala	Cys	Phe	Thr	Phe	Cys	Leu
				20					25					30
Ser	His	Gln	Asn	Leu	Lys	Glu	Phe	Ala	Leu	Thr	Asn	Pro	Glu	Lys
				35					40					45
Ser	Ser	Thr	Lys	Glu	Thr	Glu	Arg	Lys	Glu	Thr	Lys	Ala	Glu	Glu
				50					55					60
Glu	Leu	Asp	Ala	Glu	Val	Leu	Glu	Val	Phe	His	Pro	Thr	His	Glu
				65					70					75
Trp	Gln	Ala	Leu	Gln	Pro	Gly	Gln	Ala	Val	Pro	Ala	Gly	Ser	His
				80					85					90
Val	Arg	Leu	Asn	Leu	Gln	Thr	Gly	Glu	Arg	Glu	Ala	Lys	Leu	Gln
				95					100					105
Tyr	Glu	Asp	Lys	Phe	Arg	Asn	Asn	Leu	Lys	Gly	Lys	Arg	Leu	Asp
				110					115					120
Ile	Asn	Thr	Asn	Thr	Tyr	Thr	Ser	Gln	Asp	Leu	Lys	Ser	Ala	Leu
				125					130					135
Ala	Lys	Phe	Lys	Glu	Gly	Ala	Glu	Met	Glu	Ser	Ser	Lys	Glu	Asp
				140					145					150
Lys	Ala	Arg	Gln	Ala	Glu	Val	Lys	Arg	Leu	Phe	Arg	Pro	Ile	Glu
				155					160					165
Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile	Glu	Thr
				170					175					180
Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser	Ser
				185					190					195
Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu
				200					205					210
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe
				215					220					225
Gly	Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro
				230					235					240
Leu	Val	Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser
				245					250					255
Ser	Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu
				260					265					270
Gln	Lys	Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala
				275					280					285
Lys	Lys	Lys	Val	Leu	Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe

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<210> 303
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 303

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				20					25					30
Arg	Val	Ile	Ile	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35					40					45
Leu	Leu	Leu	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr
				50					55					60
Asp	Arg	Ser	Asp	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly
				65					70					75
Ala	Ala	Val	Ser	Val	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr
				80					85					90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser
				95					100					105
Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val
				110					115					120
Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	Val	Phe	Ser	Val	Ile
				125					130					135
Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	Val	Gly	Ile	His
				140					145					150
Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	Leu	Thr	Ala
				155					160					165
Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	Phe	Asp
				170					175					180
Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	Gly
				185					190					195
Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr
				200					205					210
Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly
				215					220					225
Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln
				230					235					240
Arg	Ser	Leu	Leu	Cys	Lys	Asp								
				245										

<210> 304
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
<222> 108, 123, 126, 154, 198, 206, 217
<223> unknown base

<400> 304
aagctgggttt aaggaagcag aggaggggta gattcgttga gtgaggacgg 50
aagatcaacc catttccatt ccgccagatg gcctatgttt ctggtctctc 100
ccttcggnat catcagtggt gtnntntctg ttatcaatat tttggctgat 150
gcanttgggc caggtgtggt tgggatccat ggagactcac cctattantt 200
cctganttca gccttnttga cagcagccat tatcctgctc 240

<210> 305
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332
<223> unknown base

<400> 305
gaccgaccgt tcagatgcc cgggtccagta cggcttcctg atttttggtg 50
ctgctgtntc tgtccttcta caggaggtgt tccgctttgc ctantacaag 100
ctgcttaaga aggcagatga ggggttagca tngctgagtg aggaacggaag 150
atcacccatt tccatccgcc agatggccta tgtttntggt ntttccttcg 200
gtatcatcag tgggtgttttn tctgttatca atattttggn tgatgcantt 250
gggccaggtg tggttgggat ccatggagan tcacctatt aattcctgaa 300
ttcagccttt ntgacagcag ccattatcct gntccatacc ttttggggag 350
ttgtgttttt tgatgcctgt gagaggag 378

<210> 306
<211> 655
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1, 22, 129, 133, 184
<223> unknown base

<400> 306
ngttggagaa gtggcgcgga cnttcatttg gggtttcggt ttccccctt 50
tccctttccc cggggtcttg ggtgacattg cacgggcccc tegtggggtc 100
gcgttgccac ccacgcgga ctccccagnt ggngcgccct tcccatttgc 150
ctgtcctggt caggccccca ccccccttcc cacntgacca gccatggggg 200
ctgcggtgtt tttcggctgc actttcgtcg cgttcggccc ggccttcgcg 250

cttttcttga tcaactgtggc tggggaccog cttoegcgta tcatcctggt 300
 cgcaggggca tttttctggc tgggtctccct gctcctggcc tctgtggtct 350
 gggtcatctt ggtccatgtg accgaccggt cagatgcccg gctccagtac 400
 ggctcctga tttttgggtg tgctgtctct gtccttctac aggaggtgtt 450
 ccgctttgcc tactacaagc tgcttaagaa ggcagatgag ggggttagcat 500
 cgctgagtga ggacggaaga tcaacctctt ccatccgcc gatggcctat 550
 gtttctggtc tctccttogg tatcatcagt ggtgtcttct ctgttatcaa 600
 tattttggct gatgcacttg ggccaggtgt ggttgggatc catggagact 650
 ccccc 655

<210> 307
 <211> 650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 52, 89, 128
 <223> unknown base

<400> 307
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 cnttccccgg ggtctggggg tgacattgca ccgcgccct cgtggggctcg 100
 cgttgccacc ccacgcgga tccccagntg gcgcgccct cccatttgcc 150
 tgcctggtc agggcccccac ccccttccc acctgaccag ccatgggggc 200
 tgcggtgtt ttcgggctgc actttcgtcg cgttcggggc cggccttcgc 250
 gcttttcttg atcaactgtg ctgggggacc gcttcgcgtt atcatcctgg 300
 tcgcaggggc atttttctgg ctgggtctcc tgctcctggc ctctgtggtc 350
 tggttcatct tgggtccatgt gaccgaccgg tcagatgcc ggctccagta 400
 cggcctcctg atttttgggt ctgctgtctc tgctcttcta caggaggtgt 450
 tccgctttgc ctactacaag ctgcttaaga aggcagatga ggggttagca 500
 tcgctgagtg aggacggaag atcaccatc tccatccgcc agatggccta 550
 tgtttctggt ctctccttgg gtatcatcag tgggtgtctt tctgttatca 600
 atattttggc tgatgcactt gggccaggtg tggttgggat ccatggagac 650

<210> 308
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 308
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aggaggaggc agtggccagg aaggcacagg cctgagaagt ctgcggctga 100
gctgggagca aatccccac cccctacctg ggggacaggg caagtgagac 150
ctggtgaggg tggctcagca ggcagggaag gagaggtgtc tgtgcgtcct 200
gcaccacat ctttctctgt cccctccttg ccctgtctgg aggctgctag 250
actcctatct tctgaattct atagtgcctg ggtctcagcg cagtgccgat 300
ggtggcccggt ccttgtggtt cctctctacc tggggaaata aggtgcagcg 350
gccatggcta cagcaagacc cccctggatg tgggtgctct gtgctctgat 400
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taaagatgtc agaccatca acgtctctc tcattgtccc tctgctggga 900
caaagtgtt ggtgtctggc tgggggacaa ccaagagccc ccaagtgcac 950
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gtctgcaatg gctccctgca gggactcgtg tcttggggag attacccttg 1150
tgcccgcccc aacagaccgg gtgtctacac gaacctctgc aagttcacca 1200
agtggatcca ggaaaccatc caggccaact cctgagtcac cccaggactc 1250
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agaccctcat tcttccag agatgttgag aatgttcac tctccagccc 1350
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accgtgtctc tctagttgaa ccctgggaac aatttccaaa actgtccagg 1450
gcgggggttg ogtctcaatc tccctggggc actttcatcc tcaagctcag 1500
ggcccatccc ttctctgcag ctctgacca aatttagtcc cagaaataaa 1550
ctgagaagtg gaaaaaaaaa 1570

<210> 309

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Met Ala Thr Ala Arg Pro Pro Trp Met Trp Val Leu Cys Ala Leu
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Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly
35 40 45

Ser Asn Gln Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser
50 55 60

Asp Asp Ser Ser Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met
65 70 75

His Thr Gln Pro Trp Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln
80 85 90

Leu Tyr Cys Gly Ala Val Leu Val His Pro Gln Trp Leu Leu Thr
95 100 105

Ala Ala His Cys Arg Lys Lys Val Phe Arg Val Arg Leu Gly His
110 115 120

Tyr Ser Leu Ser Pro Val Tyr Glu Ser Gly Gln Gln Met Phe Gln
125 130 135

Gly Val Lys Ser Ile Pro His Pro Gly Tyr Ser His Pro Gly His
140 145 150

Ser Asn Asp Leu Met Leu Ile Lys Leu Asn Arg Arg Ile Arg Pro
155 160 165

Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser His Cys Pro Ser
170 175 180

Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr Thr Lys Ser
185 190 195

Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn Ile Ser
200 205 210

Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln Ile
215 220 225

Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser
230 235 240

Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu
245 250 255

Gln Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn
260 265 270

Arg Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile
275 280 285

Gln Glu Thr Ile Gln Ala Asn Ser

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ccgtgctgct ggccctggct gtgctgctgg ctgtagctgt caccgggtgcc 150
gtgctcttcc tgaaccacgc ccacgcgcgc ggcacggcgc cccacactgt 200
cgtcagcact ggggctgcca gcgccaacag cgccctggtc actgtggaaa 250
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<210> 314
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 314
 Met Val Asn Asp Arg Trp Lys Thr Met Gly Gly Ala Ala Gln Leu
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 Glu Asp Arg Pro Arg Asp Lys Pro Gln Arg Pro Ser Cys Gly Tyr
 20 25 30
 Val Leu Cys Thr Val Leu Leu Ala Leu Ala Val Leu Leu Ala Val
 35 40 45
 Ala Val Thr Gly Ala Val Leu Phe Leu Asn His Ala His Ala Pro
 50 55 60
 Gly Thr Ala Pro Pro Pro Val Val Ser Thr Gly Ala Ala Ser Ala
 65 70 75
 Asn Ser Ala Leu Val Thr Val Glu Arg Ala Asp Ser Ser His Leu
 80 85 90
 Ser Ile Leu Ile Asp Pro Arg Cys Pro Asp Leu Thr Asp Ser Phe
 95 100 105

Ala Arg Leu Glu Ser	Ala Gln Ala Ser	Val Leu Gln Ala Leu Thr	110	115	120
Glu His Gln Ala Gln	Pro Arg Leu Val	Gly Asp Gln Glu Gln Glu	125	130	135
Leu Leu Asp Thr Leu	Ala Asp Gln Leu	Pro Arg Leu Leu Ala Arg	140	145	150
Ala Ser Glu Leu Gln	Thr Glu Cys Met	Gly Leu Arg Lys Gly His	155	160	165
Gly Thr Leu Gly Gln	Gly Leu Ser Ala	Leu Gln Ser Glu Gln Gly	170	175	180
Arg Leu Ile Gln Leu	Leu Ser Glu Ser	Gln Gly His Met Ala His	185	190	195
Leu Val Asn Ser Val	Ser Asp Ile Leu	Asp Ala Leu Gln Arg Asp	200	205	210
Arg Gly Leu Gly Arg	Pro Arg Asn Lys	Ala Asp Leu Gln Arg Ala	215	220	225
Pro Ala Arg Gly Thr	Arg Pro Arg Gly	Cys Ala Thr Gly Ser Arg	230	235	240
Pro Arg Asp Cys Leu	Asp Val Leu Leu	Ser Gly Gln Gln Asp Asp	245	250	255
Gly Val Tyr Ser Val	Phe Pro Thr His	Tyr Pro Ala Gly Phe Gln	260	265	270
Val Tyr Cys Asp Met	Arg Thr Asp Gly	Gly Gly Trp Thr Val Phe	275	280	285
Gln Arg Arg Glu Asp	Gly Ser Val Asn	Phe Phe Arg Gly Trp Asp	290	295	300
Ala Tyr Arg Asp Gly	Phe Gly Arg Leu	Thr Gly Glu His Trp Leu	305	310	315
Gly Leu Lys Arg Ile	His Ala Leu Thr	Thr Gln Ala Ala Tyr Glu	320	325	330
Leu His Val Asp Leu	Glu Asp Phe Glu	Asn Gly Thr Ala Tyr Ala	335	340	345
Arg Tyr Gly Ser Phe	Gly Val Gly Leu	Phe Ser Val Asp Pro Glu	350	355	360
Glu Asp Gly Tyr Pro	Leu Thr Val Ala	Asp Tyr Ser Gly Thr Ala	365	370	375
Gly Asp Ser Leu Leu	Lys His Ser Gly	Met Arg Phe Thr Thr Lys	380	385	390
Asp Arg Asp Ser Asp	His Ser Glu Asn	Asn Cys Ala Ala Phe Tyr	395	400	405
Arg Gly Ala Trp Trp	Tyr Arg Asn Cys	His Thr Ser Asn Leu Asn	410	415	420

Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val
425 430 435

Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser
440 445 450

Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
455 460

<210> 315
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 315
cacacgtcca acctcaatgg gcag 24

<210> 316
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
gaccagcagg gccaaaggaca agg 23

<210> 317
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
gttctctgag atgaagatcc ggccggtccg ggagtaccgc ttag 44

<210> 318
<211> 1841
<212> DNA
<213> Homo sapiens

<400> 318
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ggcaatccga ccacatttca ctctcaccgc ttaggaatc cagatgcagg 150
ccaagtacag cagcagcagg gacatgctgg atgatgatgg ggacaccacc 200
atgagcctgc attctcaagc ctctgccaca actcggcatc cagagccccg 250
gcgcacagag cacagggctc cctcttcaac gtggcgacca gtggccctga 300
ccctgctgac tttgtgcttg gtgctgctga tagggctggc agccctgggg 350
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<400> 319

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp
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Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
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Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser
35 40 45

Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val
50 55 60

Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr
65 70 75

Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu
80 85 90

Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val
95 100 105

Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys
110 115 120

Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser
125 130 135

Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
140 145 150

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
155 160 165

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp
170 175 180

Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser
185 190 195

Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu
200 205 210

Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
215 220 225

Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys
245 250 255

Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His
260 265 270

Val Pro Pro Glu Thr Leu Gly Glu Gly Asp
275 280

<210> 320

<211> 468

<212> DNA

<213> Homo sapiens

<220>
<221> unsure
<222> 59, 95, 149, 331, 364, 438, 446
<223> unknown base

<400> 320
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gggacatgnt ggatgatgat gggacaccac catgagcctg cattntcaag 100
cttttgccac aattcggcat ccagagcccc ggcgcacaga gcacagggnt 150
cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200
ggtgctgctg atagggctgg cagccctggg gcttttgitt tttcagtact 250
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ttaggaaata cgtcccaaga gttgcaattt nttcaagtcc agaataataa 350
gcttgcagga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400
ataacaaagc tggaggaact ttgaaggagg gcaaagtntc ctcatntact 450
atacacacac cacttccc 468

<210> 321
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 321
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<210> 322
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 322
catgctgacg acttctctgca agc 23

<210> 323
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 323
ccacacagtc tctgcttctt ggg 23

<210> 324
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
atgctggatg atgatgggga caccaccatg agcctgcatt 40

<210> 325
<211> 2988
<212> DNA
<213> Homo sapiens

<400> 325
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gagggagcgg gcccgccgcg ggggcccag ccctccggat ccgccccctc 150
cccgggtccc cccctcggga gactcctctg gctgctctgg gggttcgccg 200
gggccgggga cccgcgggtcc gggcgccatg cgggcatcgc tgctgctgtc 250
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catcagcacg gagctgggca tcaggcagag gctgctgggt gcggtgctga 600
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gatccagaat accagccatc tggccgttga tggggaccgg gcagctgctt 1350
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 ttctggggac agctctagag gagctgaacc gccgctacca cccggccttg 1550
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 ccgggggatg gaatacacgc tggacttgca gctggaggca ctgaccccc 1650
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 ccctcaccac tgcgccctcat ggatctactc tccaagaagc acccgctgga 2050
 cacactgttc ctgctggccg ggccagacac ggtgctcacg cctgaattcc 2100
 tgaaccgctg ccgcatgcat gccatctccg gctggcaggc cttctttccc 2150
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 gccccagag ctggggccgtg aactggccg ctttgatcgc caggcagcca 2250
 gcgaggcctg cttctacaac tccgactacg tggcagcccg tgggcgcctg 2300
 gcggcagcct cagaacaaga agaggagctg ctggagagcc tggatgtgta 2350
 cgagctgttc ctocacttct ccagtctgca tgtgctgcgg gcggtggagc 2400
 cggcgctgct gcagcgctac cgggcccaga cgtgcagcgc gaggctcagt 2450
 gaggacctgt accacgctg cctccagagc gtgcttgagg gcctcggtc 2500
 ccgaacccag ctggccatgc tactctttga acaggagcag ggcaacagca 2550
 cctgaccca cctgtcccc gtgggcctg gcatggccac accccacccc 2600
 attctcccc caaaaccaga gccacctgcc agcctcgctg ggcagggtg 2650
 gccgtagcca gacccaagc tggcccactg gtcccctctc tggctctgtg 2700
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 gctgtggcct ccacgtatct atgcagtaca gtctgcctga cgccagccct 2850
 gcctctgggc cctgggggct gggctgtaga agagtgttg gggaaggagg 2900

Val	Ser	Ala	Arg	Pro 275	Asp	Glu	Trp	Leu	Gly 280	Arg	Cys	Ile	Leu	Asp 285
Ala	Thr	Gly	Val	Gly 290	Cys	Thr	Gly	Asp	His 295	Glu	Gly	Val	His	Tyr 300
Ser	His	Leu	Glu	Leu 305	Ser	Pro	Gly	Glu	Pro 310	Val	Gln	Glu	Gly	Asp 315
Pro	His	Phe	Arg	Ser 320	Ala	Leu	Thr	Ala	His 325	Pro	Val	Arg	Asp	Pro 330
Val	His	Met	Tyr	Gln 335	Leu	His	Lys	Ala	Phe 340	Ala	Arg	Ala	Glu	Leu 345
Glu	Arg	Thr	Tyr	Gln 350	Glu	Ile	Gln	Glu	Leu 355	Gln	Trp	Glu	Ile	Gln 360
Asn	Thr	Ser	His	Leu 365	Ala	Val	Asp	Gly	Asp 370	Arg	Ala	Ala	Ala	Trp 375
Pro	Val	Gly	Ile	Pro 380	Ala	Pro	Ser	Arg	Pro 385	Ala	Ser	Arg	Phe	Glu 390
Val	Leu	Arg	Trp	Asp 395	Tyr	Phe	Thr	Glu	Gln 400	His	Ala	Phe	Ser	Cys 405
Ala	Asp	Gly	Ser	Pro 410	Arg	Cys	Pro	Leu	Arg 415	Gly	Ala	Asp	Arg	Ala 420
Asp	Val	Ala	Asp	Val 425	Leu	Gly	Thr	Ala	Leu 430	Glu	Glu	Leu	Asn	Arg 435
Arg	Tyr	His	Pro	Ala 440	Leu	Arg	Leu	Gln	Lys 445	Gln	Gln	Leu	Val	Asn 450
Gly	Tyr	Arg	Arg	Phe 455	Asp	Pro	Ala	Arg	Gly 460	Met	Glu	Tyr	Thr	Leu 465
Asp	Leu	Gln	Leu	Glu 470	Ala	Leu	Thr	Pro	Gln 475	Gly	Gly	Arg	Arg	Pro 480
Leu	Thr	Arg	Arg	Val 485	Gln	Leu	Leu	Arg	Pro 490	Leu	Ser	Arg	Val	Glu 495
Ile	Leu	Pro	Val	Pro 500	Tyr	Val	Thr	Glu	Ala 505	Ser	Arg	Leu	Thr	Val 510
Leu	Leu	Pro	Leu	Ala 515	Ala	Ala	Glu	Arg	Asp 520	Leu	Ala	Pro	Gly	Phe 525
Leu	Glu	Ala	Phe	Ala 530	Thr	Ala	Ala	Leu	Glu 535	Pro	Gly	Asp	Ala	Ala 540
Ala	Ala	Leu	Thr	Leu 545	Leu	Leu	Leu	Tyr	Glu 550	Pro	Arg	Gln	Ala	Gln 555
Arg	Val	Ala	His	Ala 560	Asp	Val	Phe	Ala	Pro 565	Val	Lys	Ala	His	Val 570
Ala	Glu	Leu	Glu	Arg 575	Arg	Phe	Pro	Gly	Ala 580	Arg	Val	Pro	Trp	Leu 585

Ser Val Gln Thr	Ala Ala Pro Ser Pro	Leu Arg Leu Met Asp Leu	590	595	600
Leu Ser Lys Lys	His Pro Leu Asp Thr	Leu Phe Leu Leu Ala Gly	605	610	615
Pro Asp Thr Val	Leu Thr Pro Asp Phe	Leu Asn Arg Cys Arg Met	620	625	630
His Ala Ile Ser	Gly Trp Gln Ala Phe	Phe Pro Met His Phe Gln	635	640	645
Ala Phe His Pro	Gly Val Ala Pro Pro	Gln Gly Pro Gly Pro Pro	650	655	660
Glu Leu Gly Arg	Asp Thr Gly Arg Phe	Asp Arg Gln Ala Ala Ser	665	670	675
Glu Ala Cys Phe	Tyr Asn Ser Asp Tyr	Val Ala Ala Arg Gly Arg	680	685	690
Leu Ala Ala Ala	Ser Glu Gln Glu Glu	Glu Leu Leu Glu Ser Leu	695	700	705
Asp Val Tyr Glu	Leu Phe Leu His Phe	Ser Ser Leu His Val Leu	710	715	720
Arg Ala Val Glu	Pro Ala Leu Leu Gln	Arg Tyr Arg Ala Gln Thr	725	730	735
Cys Ser Ala Arg	Leu Ser Glu Asp Leu	Tyr His Arg Cys Leu Gln	740	745	750
Ser Val Leu Glu	Gly Leu Gly Ser Arg	Thr Gln Leu Ala Met Leu	755	760	765
Leu Phe Glu Gln	Glu Gln Gly Asn Ser	Thr	770	775	

<210> 327

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 327

tggaaggctg ccgcaacgac aatc 24

<210> 328

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 328

ctgatgtggc cgatgttctg 20

<210> 329

<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 329
atggctcagt gtgcagacag 20

<210> 330
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 330
gcatgctgct ccgtgaagta gtcc 24

<210> 331
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 331
atgcatggga aagaaggcct gccc 24

<210> 332
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 333
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 333
gctctggccg gccccggcga ttggtcaccg cccgctaggg gacagccctg 50
gcctcctctg attggcaagc gctggccacc tccccacacc ccttgccaac 100
gtccccctag tggagaaaag gagtagctat tagccaattc ggcagggcc 150
gctttttaga agcttgattt cttttgaaga tgaaagacta gcggaagctc 200
tgcctctttc ccagtgggc gaggggaactc ggggcgattg gctgggaact 250
gtatccaccc aaatgtcacc gatttcttcc tatgcaggaa atgagcagac 300
ccatcaataa gaaatttctc agcctggccg aaaatggttg gccccacgaa 350
gccacgacaa ctggaggcaa agagggttgc tcaacgcccc gcctcattgg 400

aaaaccaa at cagatctggg acctatatag cgtggcggag gcggggcgat 450
 gattgtcgcg ctgcaccca ctgcagctgc gcacagtcgc atttctttcc 500
 ccgcccctga gaccctgcag caccatctgt catggcgggt gggctgtttg 550
 gtttgagcgc tcgcctcttt ttggcggcag cggcgacgcg agggctcccc 600
 gccgcccgcg tccgctggga atctagcttc tccaggactg tggtcgcccc 650
 gtccgctgtg gcgggaaagc ggccccaga accgaccaca ccgtggcaag 700
 aggaccacaga acccgaggac gaaaacttgt atgagaagaa cccagactcc 750
 catggttatg acaaggaccc cgttttggac gtctggaaca tgcgacttgt 800
 cttctttcttt ggcgtctcca tcctcttgtt ccttggcagc acctttgtgg 850
 cctatctgcc tgactacagg atgaaagagt ggtcccgcgc cgaagctgag 900
 aggccttgtga aataccgaga ggccaatggc cttcccatca tggaatccaa 950
 ctgcttcgac cccagcaaga tccagctgcc agaggatgag tgaccagttg 1000
 ctaagtgggg ctcaagaagc accgccttcc ccaccccctg cctgccattc 1050
 tgacctcttc tcagagcacc taattaaagg ggctgaaagt ctgaa 1095

<210> 334

<211> 153

<212> PRT

<213> Homo sapiens

<400> 334

Met	Ala	Ala	Gly	Leu	Phe	Gly	Leu	Ser	Ala	Arg	Arg	Leu	Leu	Ala	1	5	10	15
Ala	Ala	Ala	Thr	Arg	Gly	Leu	Pro	Ala	Ala	Arg	Val	Arg	Trp	Glu	20	25	30	
Ser	Ser	Phe	Ser	Arg	Thr	Val	Val	Ala	Pro	Ser	Ala	Val	Ala	Gly	35	40	45	
Lys	Arg	Pro	Pro	Glu	Pro	Thr	Thr	Pro	Trp	Gln	Glu	Asp	Pro	Glu	50	55	60	
Pro	Glu	Asp	Glu	Asn	Leu	Tyr	Glu	Lys	Asn	Pro	Asp	Ser	His	Gly	65	70	75	
Tyr	Asp	Lys	Asp	Pro	Val	Leu	Asp	Val	Trp	Asn	Met	Arg	Leu	Val	80	85	90	
Phe	Phe	Phe	Gly	Val	Ser	Ile	Ile	Leu	Val	Leu	Gly	Ser	Thr	Phe	95	100	105	
Val	Ala	Tyr	Leu	Pro	Asp	Tyr	Arg	Met	Lys	Glu	Trp	Ser	Arg	Arg	110	115	120	
Glu	Ala	Glu	Arg	Leu	Val	Lys	Tyr	Arg	Glu	Ala	Asn	Gly	Leu	Pro	125	130	135	
Ile	Met	Glu	Ser	Asn	Cys	Phe	Asp	Pro	Ser	Lys	Ile	Gln	Leu	Pro	140	145	150	

Glu Asp Glu

<210> 335
<211> 442
<212> DNA
<213> Homo sapiens

<400> 335
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cgacgcgagg gctcccggcc gcccgcgctc gctgggaatc tagcttctcc 100
aggactgtgg tcgccccgtc cgctgtggcg ggaaagcggc cccagaacc 150
gaccacaccg tggcaagagg acccagaacc cgaggacgaa aacttgtatg 200
agaagaaccc agactcccat ggttatgaca aggaccccggt tttggacgtc 250
tggaacatgc gacttgtctt cttctttggc gtctccatca tcctggctct 300
tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtgg 350
ccgcccgcga agctgagagg cttgtgaaat accgagaggc caatggcctt 400
cccatcatgg aatccaactg cttcgacccc agcaagatcc ag 442

<210> 336
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 336
ctgagaccct gcagaccat ctg 23

<210> 337
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 337
ggtgcttctt gagccccact tagc 24

<210> 338
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 338
aatctagctt ctccaggact gtggtcgccc cgtccgctgt 40

<210> 339
<211> 2162
<212> DNA

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	16
Income	15.5	5.5	10	30
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Depression score	0.5	0.5	0	1
Anxiety score	0.5	0.5	0	1
Overall health score	0.5	0.5	0	1

gcggcggtcta	tgccgcttgc	tctgtctgtc	ctgttgctcc	tggggcccg	50
cggctggtgc	cttgacagaac	ccccacgcga	cagcctgcgg	gaggaacttg	100
tcatcacccc	gctgccttcc	ggggacgtag	ccgccacatt	ccagttccgc	150
acgcgctggg	attcggagct	tcagcgggaa	ggagtgtccc	attacaggct	200
ctttcccaaa	gccctggggc	agctgatctc	caagtattct	ctacgggagc	250
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aaaaaaaa aa 2162

<210> 340
<211> 574
<212> PRT
<213> Homo sapiens

<400> 340
Met Pro Leu Ala Leu Leu Val Leu Leu Leu Leu Gly Pro Gly Gly
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Trp Cys Leu Ala Glu Pro Pro Arg Asp Ser Leu Arg Glu Glu Leu
20 25 30
Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala Thr Phe Gln
35 40 45
Phe Arg Thr Arg Trp Asp Ser Glu Leu Gln Arg Glu Gly Val Ser
50 55 60
His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser Lys
65 70 75
Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
80 85 90
Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly
95 100 105
Ala Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp
110 115 120
Lys Ser Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys
125 130 135
Ala Ser Leu Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr
140 145 150

Ala	Ser	Phe	Lys	Pro 155	Leu	Gly	Leu	Ala	Asn 160	Asp	Thr	Asp	His	Tyr 165
Phe	Leu	Arg	Tyr	Ala 170	Val	Leu	Pro	Arg	Glu 175	Val	Val	Cys	Thr	Glu 180
Asn	Leu	Thr	Pro	Trp 185	Lys	Lys	Leu	Leu	Pro 190	Cys	Ser	Ser	Lys	Ala 195
Gly	Leu	Ser	Val	Leu 200	Leu	Lys	Ala	Asp	Arg 205	Leu	Phe	His	Thr	Ser 210
Tyr	His	Ser	Gln	Ala 215	Val	His	Ile	Arg	Pro 220	Val	Cys	Arg	Asn	Ala 225
Arg	Cys	Thr	Ser	Ile 230	Ser	Trp	Glu	Leu	Arg 235	Gln	Thr	Leu	Ser	Val 240
Val	Phe	Asp	Ala	Phe 245	Ile	Thr	Gly	Gln	Gly 250	Lys	Lys	Asp	Trp	Ser 255
Leu	Phe	Arg	Met	Phe 260	Ser	Arg	Thr	Leu	Thr 265	Glu	Pro	Cys	Pro	Leu 270
Ala	Ser	Glu	Ser	Arg 275	Val	Tyr	Val	Asp	Ile 280	Thr	Thr	Tyr	Asn	Gln 285
Asp	Asn	Glu	Thr	Leu 290	Glu	Val	His	Pro	Pro 295	Pro	Thr	Thr	Thr	Tyr 300
Gln	Asp	Val	Ile	Leu 305	Gly	Thr	Arg	Lys	Thr 310	Tyr	Ala	Ile	Tyr	Asp 315
Leu	Leu	Asp	Thr	Ala 320	Met	Ile	Asn	Asn	Ser 325	Arg	Asn	Leu	Asn	Ile 330
Gln	Leu	Lys	Trp	Lys 335	Arg	Pro	Pro	Glu	Asn 340	Glu	Ala	Pro	Pro	Val 345
Pro	Phe	Leu	His	Ala 350	Gln	Arg	Tyr	Val	Ser 355	Gly	Tyr	Gly	Leu	Gln 360
Lys	Gly	Glu	Leu	Ser 365	Thr	Leu	Leu	Tyr	Asn 370	Thr	His	Pro	Tyr	Arg 375
Ala	Phe	Pro	Val	Leu 380	Leu	Leu	Asp	Thr	Val 385	Pro	Trp	Tyr	Leu	Arg 390
Leu	Tyr	Val	His	Thr 395	Leu	Thr	Ile	Thr	Ser 400	Lys	Gly	Lys	Glu	Asn 405
Lys	Pro	Ser	Tyr	Ile 410	His	Tyr	Gln	Pro	Ala 415	Gln	Asp	Arg	Leu	Gln 420
Pro	His	Leu	Leu	Glu 425	Met	Leu	Ile	Gln	Leu 430	Pro	Ala	Asn	Ser	Val 435
Thr	Lys	Val	Ser	Ile 440	Gln	Phe	Glu	Arg	Ala 445	Leu	Leu	Lys	Trp	Thr 450
Glu	Tyr	Thr	Pro	Asp 455	Pro	Asn	His	Gly	Phe 460	Tyr	Val	Ser	Pro	Ser 465

Val Leu Ser Ala Leu Val Pro Ser Met Val Ala Ala Lys Pro Val
470 475 480

Asp Trp Glu Glu Ser Pro Leu Phe Asn Ser Leu Phe Pro Val Ser
485 490 495

Asp Gly Ser Asn Tyr Phe Val Arg Leu Tyr Thr Glu Pro Leu Leu
500 505 510

Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr Asn Val Ile
515 520 525

Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser Phe Tyr
530 535 540

Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Arg Thr Gly
545 550 555

Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly
560 565 570

Val Pro Pro Leu

<210> 341
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
tggacaccgt accctggtat ctgc 24

<210> 342
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic oligonucleotide probe

<400> 342
ccaactctga ggagagcaag tggc 24

<210> 343
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 343
tgtatgtgca caccctcacc atcacctcca agggcaagga gaac 44

<210> 344
<211> 762
<212> DNA
<213> Homo sapiens

<400> 344
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 gtttggccag ctgacaacgt acgctgcttc aagtccgata cccccagtg 150
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 aaggatgaag atgtgtcaag gccataccct gagccaggat gggaggccaa 300
 gtgtccaggc tcctcctcta ccagggtgtcc tcagaaatga tgctgggtcc 350
 tttctacctc tgggggtcac tctcacttgg cacctgcccc tgaggggtcct 400
 gagacttgga atatggaaga agcaataccc aacccaccca aagaaaacct 450
 gagcttgaag tccttttccc caaaaagagg gaagagtcac aaaaagtcca 500
 gaccccgagg acggtacttt ccctctctac ctggtgtctcc tccctaattgc 550
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 aaagagctgc cttgcccttc tgcaatgtgt gatcacagct agaaggcact 650
 gtcagagaag agaaactggc cctcaccaga tgctgaatct gctgggtgcct 700
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 tttataatcc aa 762

<210> 345
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 345
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 Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys
 20 25 30
 Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp
 35 40 45
 Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys
 50 55 60
 Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys
 65 70 75
 Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro
 80 85 90
 Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser
 95 100 105
 Thr Arg Cys Pro Gln Lys
 110

Variable	Mean	SD	Min	Max
Age	45.1	10.2	25	65
Gender	Male	10.1	0	10
Marital status	Married	10.1	0	10
Education	High school	10.1	0	10
Occupation	Manager	10.1	0	10
Income	\$50,000	10.1	0	10
Health status	Good	10.1	0	10
Exercise frequency	Weekly	10.1	0	10
Dietary habits	Healthy	10.1	0	10
Stress level	Low	10.1	0	10
Sleep quality	Good	10.1	0	10
Mental health	Stable	10.1	0	10
Life satisfaction	High	10.1	0	10
Work-life balance	Good	10.1	0	10
Family support	Strong	10.1	0	10
Community involvement	Active	10.1	0	10
Personal growth	High	10.1	0	10
Resilience	High	10.1	0	10
Emotional stability	High	10.1	0	10
Self-awareness	High	10.1	0	10
Empathy	High	10.1	0	10
Communication skills	High	10.1	0	10
Problem-solving abilities	High	10.1	0	10
Decision-making skills	High	10.1	0	10
Time management	High	10.1	0	10
Organization skills	High	10.1	0	10
Leadership skills	High	10.1	0	10
Teamwork skills	High	10.1	0	10
Conflict resolution	High	10.1	0	10
Networking skills	High	10.1	0	10
Adaptability	High	10.1	0	10
Flexibility	High	10.1	0	10
Open-mindedness	High	10.1	0	10
Creativity	High	10.1	0	10
Innovation	High	10.1	0	10
Risk-taking	High	10.1	0	10
Perseverance	High	10.1	0	10
Patience	High	10.1	0	10
Self-discipline	High	10.1	0	10
Goal setting	High	10.1	0	10
Time management	High	10.1	0	10
Organization skills	High	10.1	0	10
Leadership skills	High	10.1	0	10
Teamwork skills	High	10.1	0	10
Conflict resolution	High	10.1	0	10
Networking skills	High	10.1	0	10
Adaptability	High	10.1	0	10
Flexibility	High	10.1	0	10
Open-mindedness	High	10.1	0	10
Creativity	High	10.1	0	10
Innovation	High	10.1	0	10
Risk-taking	High	10.1	0	10
Perseverance	High	10.1	0	10
Patience	High	10.1	0	10
Self-discipline	High	10.1	0	10
Goal setting	High	10.1	0	10

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 <212> PRT
 <213> Homo sapiens

<400> 347
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 Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His
 35 40 45
 Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala
 50 55 60
 Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

				65					70					75
Tyr	Ala	Glu	Pro	Ala 80	Pro	Glu	Asn	Asn	Ala 85	Leu	Asn	Thr	Gln	Thr 90
Gln	Pro	Lys	Ala	His 95	Thr	Thr	Gly	Asp	Arg 100	Gly	Lys	Glu	Ala	Asn 105
Gln	Ala	Pro	Pro	Glu 110	Glu	Gln	Asp	Lys	Val 115	Pro	His	Thr	Ala	Gln 120
Arg	Ala	Ala	Trp	Lys 125	Ser	Pro	Glu	Lys	Glu 130	Lys	Thr	Met	Val	Asn 135
Thr	Leu	Ser	Pro	Arg 140	Gly	Gln	Asp	Ala	Gly 145	Met	Ala	Ser	Gly	Arg 150
Thr	Glu	Ala	Gln	Ser 155	Trp	Lys	Ser	Gln	Asp 160	Thr	Lys	Thr	Thr	Gln 165
Gly	Asn	Gly	Gly	Gln 170	Thr	Arg	Lys	Leu	Thr 175	Ala	Ser	Arg	Thr	Val 180
Ser	Glu	Lys	His	Gln 185	Gly	Lys	Ala	Ala	Thr 190	Thr	Ala	Lys	Thr	Leu 195
Ile	Pro	Lys	Ser	Gln 200	His	Arg	Met	Leu	Ala 205	Pro	Thr	Gly	Ala	Val 210
Ser	Thr	Arg	Thr	Arg 215	Gln	Lys	Gly	Val	Thr 220	Thr	Ala	Val	Ile	Pro 225
Pro	Lys	Glu	Lys	Lys 230	Pro	Gln	Ala	Thr	Pro 235	Pro	Pro	Ala	Pro	Phe 240
Gln	Ser	Pro	Thr	Thr 245	Gln	Arg	Asn	Gln	Arg 250	Leu	Lys	Ala	Ala	Asn 255
Phe	Lys	Ser	Glu	Pro 260	Arg	Trp	Asp	Phe	Glu 265	Glu	Lys	Tyr	Ser	Phe 270
Glu	Ile	Gly	Gly	Leu 275	Gln	Thr	Thr	Cys	Pro 280	Asp	Ser	Val	Lys	Ile 285
Lys	Ala	Ser	Lys	Ser 290	Leu	Trp	Leu	Gln	Lys 295	Leu	Phe	Leu	Pro	Asn 300
Leu	Thr	Leu	Phe	Leu 305	Asp	Ser	Arg	His	Phe 310	Asn	Gln	Ser	Glu	Trp 315
Asp	Arg	Leu	Glu	His 320	Phe	Ala	Pro	Pro	Phe 325	Gly	Phe	Met	Glu	Leu 330
Asn	Tyr	Ser	Leu	Val 335	Gln	Lys	Val	Val	Thr 340	Arg	Phe	Pro	Pro	Val 345
Pro	Gln	Gln	Gln	Leu 350	Leu	Leu	Ala	Ser	Leu 355	Pro	Ala	Gly	Ser	Leu 360
Arg	Cys	Ile	Thr	Cys 365	Ala	Val	Val	Gly	Asn 370	Gly	Gly	Ile	Leu	Asn 375
Asn	Ser	His	Met	Gly	Gln	Glu	Ile	Asp	Ser	His	Asp	Tyr	Val	Phe

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<210> 349
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 349
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 35 40 45
 Tyr Phe Ser Pro Lys Cys Ser Lys His Phe His Arg Leu Tyr His
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 Asn Thr Arg Asp Cys Thr Ile Pro Ala Tyr Tyr Lys Arg Cys Ala
 65 70 75
 Arg Leu Leu Thr Arg Leu Ala Val Ser Pro Val Cys Met Glu Asp
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Lys

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 <211> 1141
 <212> DNA
 <213> Homo sapiens

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<210> 351
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 351

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Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe	35	40	45	
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg	50	55	60	
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln	65	70	75	
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala	80	85	90	
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys	95	100	105	
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln	110	115	120	
Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile	125	130	135	
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly	140	145	150	
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro	155	160	165	
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn	170	175	180	

Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro
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Gly Ala

<210> 352
 <211> 3226
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 353
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 35 40 45
 Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile Pro
 50 55 60
 Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr
 65 70 75
 Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr
 80 85 90
 Ser Thr Ile Ile Leu His Ser His His Leu Gln Ile Ser Arg Ala
 95 100 105
 Thr Leu Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu
 110 115 120
 Gln Val Leu Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala
 125 130 135
 Pro Glu Pro Leu Leu Val Gly Leu Pro Tyr Thr Val Val Ile His
 140 145 150
 Tyr Ala Gly Asn Leu Ser Glu Thr Phe His Gly Phe Tyr Lys Ser
 155 160 165
 Thr Tyr Arg Thr Lys Glu Gly Glu Leu Arg Ile Leu Ala Ser Thr
 170 175 180
 Gln Phe Glu Pro Thr Ala Ala Arg Met Ala Phe Pro Cys Phe Asp
 185 190 195
 Glu Pro Ala Phe Lys Ala Ser Phe Ser Ile Lys Ile Arg Arg Glu
 200 205 210
 Pro Arg His Leu Ala Ile Ser Asn Met Pro Leu Val Lys Ser Val

215	220	225
Thr Val Ala Glu Gly Leu Ile Glu Asp	His Phe Asp Val Thr Val	
230	235	240
Lys Met Ser Thr Tyr Leu Val Ala Phe	Ile Ile Ser Asp Phe Glu	
245	250	255
Ser Val Ser Lys Ile Thr Lys Ser Gly	Val Lys Val Ser Val Tyr	
260	265	270
Ala Val Pro Asp Lys Ile Asn Gln Ala	Asp Tyr Ala Leu Asp Ala	
275	280	285
Ala Val Thr Leu Leu Glu Phe Tyr Glu	Asp Tyr Phe Ser Ile Pro	
290	295	300
Tyr Pro Leu Pro Lys Gln Asp Leu Ala	Ala Ile Pro Asp Phe Gln	
305	310	315
Ser Gly Ala Met Glu Asn Trp Gly Leu	Thr Thr Tyr Arg Glu Ser	
320	325	330
Ala Leu Leu Phe Asp Ala Glu Lys Ser	Ser Ala Ser Ser Lys Leu	
335	340	345
Gly Ile Thr Val Thr Val Ala His Glu	Leu Ala His Gln Trp Phe	
350	355	360
Gly Asn Leu Val Thr Met Glu Trp Trp	Asn Asp Leu Trp Leu Asn	
365	370	375
Glu Gly Phe Ala Lys Phe Met Glu Phe	Val Ser Val Ser Val Thr	
380	385	390
His Pro Glu Leu Lys Val Gly Asp Tyr	Phe Phe Gly Lys Cys Phe	
395	400	405
Asp Ala Met Glu Val Asp Ala Leu Asn	Ser Ser His Pro Val Ser	
410	415	420
Thr Pro Val Glu Asn Pro Ala Gln Ile	Arg Glu Met Phe Asp Asp	
425	430	435
Val Ser Tyr Asp Lys Gly Ala Cys Ile	Leu Asn Met Leu Arg Glu	
440	445	450
Tyr Leu Ser Ala Asp Ala Phe Lys Ser	Gly Ile Val Gln Tyr Leu	
455	460	465
Gln Lys His Ser Tyr Lys Asn Thr Lys	Asn Glu Asp Leu Trp Asp	
470	475	480
Ser Met Ala Ser Ile Cys Pro Thr Asp	Gly Val Lys Gly Met Asp	
485	490	495
Gly Phe Cys Ser Arg Ser Gln His Ser	Ser Ser Ser Ser His Trp	
500	505	510
His Gln Glu Gly Val Asp Val Lys Thr	Met Met Asn Thr Trp Thr	
515	520	525
Leu Gln Arg Gly Phe Pro Leu Ile Thr	Ile Thr Val Arg Gly Arg	

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Asn	Val	His	Met	Lys 545	Gln	Glu	His	Tyr	Met 550	Lys	Gly	Ser	Asp	Gly 555
Ala	Pro	Asp	Thr	Gly 560	Tyr	Leu	Trp	His	Val 565	Pro	Leu	Thr	Phe	Ile 570
Thr	Ser	Lys	Ser	Asn 575	Met	Val	His	Arg	Phe 580	Leu	Leu	Lys	Thr	Lys 585
Thr	Asp	Val	Leu	Ile 590	Leu	Pro	Glu	Glu	Val 595	Glu	Trp	Ile	Lys	Phe 600
Asn	Val	Gly	Met	Asn 605	Gly	Tyr	Tyr	Ile	Val 610	His	Tyr	Glu	Asp	Asp 615
Gly	Trp	Asp	Ser	Leu 620	Thr	Gly	Leu	Leu	Lys 625	Gly	Thr	His	Thr	Ala 630
Val	Ser	Ser	Asn	Asp 635	Arg	Ala	Ser	Leu	Ile 640	Asn	Asn	Ala	Phe	Gln 645
Leu	Val	Ser	Ile	Gly 650	Lys	Leu	Ser	Ile	Glu 655	Lys	Ala	Leu	Asp	Leu 660
Ser	Leu	Tyr	Leu	Lys 665	His	Glu	Thr	Glu	Ile 670	Met	Pro	Val	Phe	Gln 675
Gly	Leu	Asn	Glu	Leu 680	Ile	Pro	Met	Tyr	Lys 685	Leu	Met	Glu	Lys	Arg 690
Asp	Met	Asn	Glu	Val 695	Glu	Thr	Gln	Phe	Lys 700	Ala	Phe	Leu	Ile	Arg 705
Leu	Leu	Arg	Asp	Leu 710	Ile	Asp	Lys	Gln	Thr 715	Trp	Thr	Asp	Glu	Gly 720
Ser	Val	Ser	Glu	Gln 725	Met	Leu	Arg	Ser	Glu 730	Leu	Leu	Leu	Leu	Ala 735
Cys	Val	His	Asn	Tyr 740	Gln	Pro	Cys	Val	Gln 745	Arg	Ala	Glu	Gly	Tyr 750
Phe	Arg	Lys	Trp	Lys 755	Glu	Ser	Asn	Gly	Asn 760	Leu	Ser	Leu	Pro	Val 765
Asp	Val	Thr	Leu	Ala 770	Val	Phe	Ala	Val	Gly 775	Ala	Gln	Ser	Thr	Glu 780
Gly	Trp	Asp	Phe	Leu 785	Tyr	Ser	Lys	Tyr	Gln 790	Phe	Ser	Leu	Ser	Ser 795
Thr	Glu	Lys	Ser	Gln 800	Ile	Glu	Phe	Ala	Leu 805	Cys	Arg	Thr	Gln	Asn 810
Lys	Glu	Lys	Leu	Gln 815	Trp	Leu	Leu	Asp	Glu 820	Ser	Phe	Lys	Gly	Asp 825
Lys	Ile	Lys	Thr	Gln 830	Glu	Phe	Pro	Gln	Ile 835	Leu	Thr	Leu	Ile	Gly 840
Arg	Asn	Pro	Val	Gly	Tyr	Pro	Leu	Ala	Trp	Gln	Phe	Leu	Arg	Lys

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 <213> Homo sapiens

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 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
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 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
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 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
 95 100 105
 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
 110 115 120
 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
 125 130 135
 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
 140 145 150
 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu

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Pro Gln Pro Gly Cys Asn Leu Leu Asn	Gly Thr Gln Glu Ile Gly	
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Pro Val Gly Met Thr Glu Asn Cys Asn	Arg Lys Asp Phe Leu Thr	
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Cys His Arg Gly Thr Thr Ile Met Thr	His Gly Asn Leu Ala Gln	
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Glu Pro Thr Asp Trp Thr Thr Ser Asn	Thr Glu Met Cys Glu Val	
230	235	240
Gly Gln Val Cys Gln Glu Thr Leu Leu	Leu Ile Asp Val Gly Leu	
245	250	255
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260	265	270
Gln Asn Ser Gln Lys Thr Thr Ile His	Ser Ala Pro Pro Gly Val	
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Leu Val Ala Ser Tyr Thr His Phe Cys	Ser Ser Asp Leu Cys Asn	
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Pro Leu Gly Thr Cys Ser Ser Gly Ser	Pro Arg Met Thr Cys Pro	
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly	Tyr Ile His Leu Ser Gly	
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile	Gln Gly Cys Val Ala Gln	
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr	Arg Gln Ile Gly Ile Phe	
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln	Pro Pro Ala Ser Gln His	
395	400	405
Glu Gly Gly Gly Ala Glu Gly Leu Glu	Ser Leu Thr Trp Gly Val	
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 <211> 271
 <212> PRT
 <213> Homo sapiens

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Lys	Gly	Ser	Val	Gly	Arg	His	Gly	Lys	Ile	Gly	Pro	Ile	Gly	Ser	80	85	90
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly	Asp	Ile	Gly	Pro	Pro	Gly	Pro	95	100	105
Asn	Gly	Glu	Pro	Gly	Leu	Pro	Cys	Glu	Cys	Ser	Gln	Leu	Arg	Lys	110	115	120
Ala	Ile	Gly	Glu	Met	Asp	Asn	Gln	Val	Ser	Gln	Leu	Thr	Ser	Glu	125	130	135
Leu	Lys	Phe	Ile	Lys	Asn	Ala	Val	Ala	Gly	Val	Arg	Glu	Thr	Glu	140	145	150
Ser	Lys	Ile	Tyr	Leu	Leu	Val	Lys	Glu	Glu	Lys	Arg	Tyr	Ala	Asp	155	160	165
Ala	Gln	Leu	Ser	Cys	Gln	Gly	Arg	Gly	Gly	Thr	Leu	Ser	Met	Pro	170	175	180
Lys	Asp	Glu	Ala	Ala	Asn	Gly	Leu	Met	Ala	Ala	Tyr	Leu	Ala	Gln	185	190	195
Ala	Gly	Leu	Ala	Arg	Val	Phe	Ile	Gly	Ile	Asn	Asp	Leu	Glu	Lys	200	205	210
Glu	Gly	Ala	Phe	Val	Tyr	Ser	Asp	His	Ser	Pro	Met	Arg	Thr	Phe	215	220	225
Asn	Lys	Trp	Arg	Ser	Gly	Glu	Pro	Asn	Asn	Ala	Tyr	Asp	Glu	Glu	230	235	240
Asp	Cys	Val	Glu	Met	Val	Ala	Ser	Gly	Gly	Trp	Asn	Asp	Val	Ala	245	250	255
Cys	His	Thr	Thr	Met	Tyr	Phe	Met	Cys	Glu	Phe	Asp	Lys	Glu	Asn	260	265	270

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 <213> Homo sapiens

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<210> 360

<211> 1738

<212> DNA

<213> Homo sapiens

<400> 360

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<210> 361

<211> 159

<212> PRT

<213> Homo sapiens

<400> 361

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Leu	Glu	Glu	Leu	Leu	Ser	Lys	Tyr	Gln	His	Asn	Glu	Ser	His	Ser	35	40	45	
Arg	Val	Arg	Arg	Ala	Ile	Pro	Arg	Glu	Asp	Lys	Glu	Glu	Ile	Leu	50	55	60	
Met	Leu	His	Asn	Lys	Leu	Arg	Gly	Gln	Val	Gln	Pro	Gln	Ala	Ser	65	70	75	
Asn	Met	Glu	Tyr	Met	Val	Ser	Ala	Gly	Ser	Gly	Arg	Arg	Gly	Trp	80	85	90	
His	Arg	Gly	Trp	Gly	Leu	Gly	His	Gln	Pro	Ala	Leu	Phe	Pro	Ser	95	100	105	
Gln	Leu	Cys	Ser	Pro	Ala	Ser	Ala	Cys	Asp	Gly	Trp	Leu	Arg	Val	110	115	120	
Ser	Ser	Gly	Arg	Gly	Gly	Ser	Arg	Leu	Cys	Ser	Val	Leu	Phe	Val	125	130	135	
Cys	Phe	Glu	Thr	Gly	Ser	His	Ser	Ala	Thr	Asp	Ala	Gly	Val	Gln	140	145	150	
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<211> 422

<212> DNA

<213> Homo sapiens

<400> 362

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<211> 78

<213> Homo sapiens

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Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu
35 40 45

Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
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Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val
65 70 75

Cys Asn Thr

<211> 826

<213> Homo sapiens

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35 40 45
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 gtgtggagtg tttgcacatc attgaattct cgtttcacct ttgtgaaaca 2100

Table 1. Demographic characteristics of the study population	
Demographic characteristics	
Age (mean \pm SD)	65.2 \pm 10.5
Gender (male/female)	102/108
Education (years)	12.5 \pm 2.1
Marital status (married/divorced/widowed)	150/30/20
Occupation (retired/working)	150/30
Income (USD/month)	1,200 \pm 300
Health status (good/poor)	180/20
Comorbidities (hypertension/diabetes/cholesterol)	120/80/40
Medication (yes/no)	150/30
Smoking status (smoker/non-smoker)	50/130
Alcohol consumption (yes/no)	30/150
Family history (yes/no)	40/140
Genetic testing (yes/no)	100/80
Genetic testing results (normal/abnormal)	80/20
Genetic testing cost (USD)	500
Genetic testing insurance coverage (yes/no)	100/80
Genetic testing satisfaction (yes/no)	100/80
Genetic testing knowledge (yes/no)	100/80
Genetic testing awareness (yes/no)	100/80
Genetic testing interest (yes/no)	100/80
Genetic testing motivation (yes/no)	100/80
Genetic testing barriers (yes/no)	100/80
Genetic testing facilitators (yes/no)	100/80
Genetic testing outcomes (yes/no)	100/80
Genetic testing impact (yes/no)	100/80
Genetic testing future (yes/no)	100/80
Genetic testing policy (yes/no)	100/80
Genetic testing regulation (yes/no)	100/80
Genetic testing ethics (yes/no)	100/80
Genetic testing privacy (yes/no)	100/80
Genetic testing security (yes/no)	100/80
Genetic testing accuracy (yes/no)	100/80
Genetic testing reliability (yes/no)	100/80
Genetic testing validity (yes/no)	100/80
Genetic testing utility (yes/no)	100/80
Genetic testing feasibility (yes/no)	100/80
Genetic testing acceptability (yes/no)	100/80
Genetic testing desirability (yes/no)	100/80
Genetic testing morality (yes/no)	100/80
Genetic testing justice (yes/no)	100/80
Genetic testing equity (yes/no)	100/80
Genetic testing efficiency (yes/no)	100/80
Genetic testing effectiveness (yes/no)	100/80
Genetic testing impact (yes/no)	100/80
Genetic testing future (yes/no)	100/80
Genetic testing policy (yes/no)	100/80
Genetic testing regulation (yes/no)	100/80
Genetic testing ethics (yes/no)	100/80
Genetic testing privacy (yes/no)	100/80
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Genetic testing morality (yes/no)	100/80
Genetic testing justice (yes/no)	100/80
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Genetic testing efficiency (yes/no)	100/80
Genetic testing effectiveness (yes/no)	100/80
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Genetic testing desirability (yes/no)	100/80
Genetic testing morality (yes/no)	100/80
Genetic testing justice (yes/no)	100/80
Genetic testing equity (yes/no)	100/80
Genetic testing efficiency (yes/no)	100/80
Genetic testing effectiveness (yes/no)	100/80
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Genetic testing regulation (yes/no)	100/80
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Genetic testing reliability (yes/no)	100/80
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Genetic testing utility (yes/no)	100/80
Genetic testing feasibility (yes/no)	100/80
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Genetic testing desirability (yes/no)	100/80
Genetic testing morality (yes/no)	100/80
Genetic testing justice (yes/no)	100/80
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Genetic testing effectiveness (yes/no)	100/80
Genetic testing impact (yes/no)	100/80
Genetic testing future (yes/no)	100/80
Genetic testing policy (yes/no)	100/80
Genetic testing regulation (yes/no)	100/80
Genetic testing ethics (yes/no)	100/80
Genetic testing	

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Met	Val	His	Tyr	Ile 35	Tyr	Gln	Arg	Phe	Arg 40	Val	Leu	Glu	Gln	Gly 45
Leu	Glu	Lys	Cys	Thr 50	Gln	Ala	Thr	Arg	Ala 55	Tyr	Ile	Gln	Glu	Phe 60
Gln	Glu	Phe	Ser	Lys 65	Asn	Ile	Ser	Val	Met 70	Leu	Gly	Arg	Cys	Gln 75
Thr	Tyr	Thr	Ser	Glu 80	Tyr	Lys	Ser	Ala	Val 85	Gly	Asn	Leu	Ala	Leu 90
Arg	Val	Glu	Arg	Ala 95	Gln	Arg	Glu	Ile	Asp 100	Tyr	Ile	Gln	Tyr	Leu 105
Arg	Glu	Ala	Asp	Glu 110	Cys	Ile	Val	Ser	Glu 115	Asp	Lys	Thr	Leu	Ala 120
Glu	Met	Leu	Leu	Gln 125	Glu	Ala	Glu	Glu	Glu 130	Lys	Lys	Ile	Arg	Thr 135
Leu	Leu	Asn	Ala	Ser 140	Cys	Asp	Asn	Met	Leu 145	Met	Gly	Ile	Lys	Ser 150
Leu	Lys	Ile	Val	Lys 155	Lys	Met	Met	Asp	Thr 160	His	Gly	Ser	Trp	Met 165
Lys	Asp	Ala	Val	Tyr 170	Asn	Ser	Pro	Lys	Val 175	Tyr	Leu	Leu	Ile	Gly 180
Ser	Arg	Asn	Asn	Thr 185	Val	Trp	Glu	Phe	Ala 190	Asn	Ile	Arg	Ala	Phe 195
Met	Glu	Asp	Asn	Thr 200	Lys	Pro	Ala	Pro	Arg 205	Lys	Gln	Ile	Leu	Thr 210

Leu	Ser	Trp	Gln	Gly	Thr	Gly	Gln	Val	Ile	Tyr	Lys	Gly	Phe	Leu
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Phe	Phe	His	Asn	Gln	Ala	Thr	Ser	Asn	Glu	Ile	Ile	Lys	Tyr	Asn
				230					235					240
Leu	Gln	Lys	Arg	Thr	Val	Glu	Asp	Arg	Met	Leu	Leu	Pro	Gly	Gly
				245					250					255
Val	Gly	Arg	Ala	Leu	Val	Tyr	Gln	His	Ser	Pro	Ser	Thr	Tyr	Ile
				260					265					270
Asp	Leu	Ala	Val	Asp	Glu	His	Gly	Leu	Trp	Ala	Ile	His	Ser	Gly
				275					280					285
Pro	Gly	Thr	His	Ser	His	Leu	Val	Leu	Thr	Lys	Ile	Glu	Pro	Gly
				290					295					300
Thr	Leu	Gly	Val	Glu	His	Ser	Trp	Asp	Thr	Pro	Cys	Arg	Ser	Gln
				305					310					315
Asp	Ala	Glu	Ala	Ser	Phe	Leu	Leu	Cys	Gly	Val	Leu	Tyr	Val	Val
				320					325					330
Tyr	Ser	Thr	Gly	Gly	Gln	Gly	Pro	His	Arg	Ile	Thr	Cys	Ile	Tyr
				335					340					345
Asp	Pro	Leu	Gly	Thr	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Asn	Leu	Phe
				350					355					360
Phe	Pro	Lys	Arg	Pro	Arg	Ser	His	Ser	Met	Ile	His	Tyr	Asn	Pro
				365					370					375
Arg	Asp	Lys	Gln	Leu	Tyr	Ala	Trp	Asn	Glu	Gly	Asn	Gln	Ile	Ile
				380					385					390
Tyr	Lys	Leu	Gln	Thr	Lys	Arg	Lys	Leu	Pro	Leu	Lys			
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 <212> DNA
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<210> 369

<211> 447

<212> PRT

<213> Homo sapiens

<400> 369

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Trp	Leu	Arg	Ala	Gly	Glu	Glu	Arg	Ser	Gly	Arg	Pro	Ala	Cys	Gln	35	40	45	
Lys	Ala	Asn	Gly	Phe	Pro	Pro	Asp	Lys	Ser	Ser	Gly	Ser	Lys	Lys	50	55	60	
Gln	Lys	Gln	Tyr	Gln	Arg	Ile	Arg	Lys	Glu	Lys	Pro	Gln	Gln	His	65	70	75	
Asn	Phe	Thr	His	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Lys	Ser	His	Ser	80	85	90	
Gly	Asn	Ile	Ser	Cys	Met	Asp	Phe	Ser	Ser	Asn	Gly	Lys	Tyr	Leu	95	100	105	
Ala	Thr	Cys	Ala	Asp	Asp	Arg	Thr	Ile	Arg	Ile	Trp	Ser	Thr	Lys	110	115	120	
Asp	Phe	Leu	Gln	Arg	Glu	His	Arg	Ser	Met	Arg	Ala	Asn	Val	Glu	125	130	135	
Leu	Asp	His	Ala	Thr	Leu	Val	Arg	Phe	Ser	Pro	Asp	Cys	Arg	Ala	140	145	150	
Phe	Ile	Val	Trp	Leu	Ala	Asn	Gly	Asp	Thr	Leu	Arg	Val	Phe	Lys	155	160	165	
Met	Thr	Lys	Arg	Glu	Asp	Gly	Gly	Tyr	Thr	Phe	Thr	Ala	Thr	Pro	170	175	180	
Glu	Asp	Phe	Pro	Lys	Lys	His	Lys	Ala	Pro	Val	Ile	Asp	Ile	Gly	185	190	195	
Ile	Ala	Asn	Thr	Gly	Lys	Phe	Ile	Met	Thr	Ala	Ser	Ser	Asp	Thr	200	205	210	
Thr	Val	Leu	Ile	Trp	Ser	Leu	Lys	Gly	Gln	Val	Leu	Ser	Thr	Ile	215	220	225	
Asn	Thr	Asn	Gln	Met	Asn	Asn	Thr	His	Ala	Ala	Val	Ser	Pro	Cys	230	235	240	

Gly	Arg	Phe	Val	Ala	Ser	Cys	Gly	Phe	Thr	Pro	Asp	Val	Lys	Val	245	250	255
Trp	Glu	Val	Cys	Phe	Gly	Lys	Lys	Gly	Glu	Phe	Gln	Glu	Val	Val	260	265	270
Arg	Ala	Phe	Glu	Leu	Lys	Gly	His	Ser	Ala	Ala	Val	His	Ser	Phe	275	280	285
Ala	Phe	Ser	Asn	Asp	Ser	Arg	Arg	Met	Ala	Ser	Val	Ser	Lys	Asp	290	295	300
Gly	Thr	Trp	Lys	Leu	Trp	Asp	Thr	Asp	Val	Glu	Tyr	Lys	Lys	Lys	305	310	315
Gln	Asp	Pro	Tyr	Leu	Leu	Lys	Thr	Gly	Arg	Phe	Glu	Glu	Ala	Ala	320	325	330
Gly	Ala	Ala	Pro	Cys	Arg	Leu	Ala	Leu	Ser	Pro	Asn	Ala	Gln	Val	335	340	345
Leu	Ala	Leu	Ala	Ser	Gly	Ser	Ser	Ile	His	Leu	Tyr	Asn	Thr	Arg	350	355	360
Arg	Gly	Glu	Lys	Glu	Glu	Cys	Phe	Glu	Arg	Val	His	Gly	Glu	Cys	365	370	375
Ile	Ala	Asn	Leu	Ser	Phe	Asp	Ile	Thr	Gly	Arg	Phe	Leu	Ala	Ser	380	385	390
Cys	Gly	Asp	Arg	Ala	Val	Arg	Leu	Phe	His	Asn	Thr	Pro	Gly	His	395	400	405
Arg	Ala	Met	Val	Glu	Glu	Met	Gln	Gly	His	Leu	Lys	Arg	Ala	Ser	410	415	420
Asn	Glu	Ser	Thr	Arg	Gln	Arg	Leu	Gln	Gln	Gln	Leu	Thr	Gln	Ala	425	430	435
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<211> 1415

<212> DNA

<213> Homo sapiens

<400> 370

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caggttcccg gacggcaggt accgctgctc catggacttg aagaacatca 400

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<211> 105

<212> PRT

<213> Homo sapiens

<400> 371

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				20					25					30
Gln	Cys	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg
				35					40					45
Gly	Leu	Arg	Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys
				50					55					60
His	Pro	Gly	Ser	His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His
				65					70					75

[illegible]

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Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
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Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
65 70 75

Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
95 100 105

Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp
125 130 135

Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala
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Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu
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Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu Ala
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 Thr Ser Ala Asn Glu Asn Ser Thr Val Leu Pro Ser Ser Thr Ser
 35 40 45
 Ser Ser Ser Asp Gly Asn Leu Arg Pro Glu Ala Ile Thr Ala Ile
 50 55 60
 Ile Val Val Phe Ser Leu Leu Ala Ala Leu Leu Leu Ala Val Gly
 65 70 75
 Leu Ala Leu Leu Val Arg Lys Leu Arg Glu Lys Arg Gln Thr Glu
 80 85 90
 Gly Thr Tyr Arg Pro Ser Ser Glu Glu Gln Phe Ser His Ala Ala
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 Glu Ala Arg Ala Pro Gln Asp Ser Lys Glu Thr Val Gln Gly Cys
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Leu Pro Ile

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 <212> DNA
 <213> Homo sapiens

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<210> 379
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<212> PRT
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				20					25					30	
Phe	Glu	Asp	Ile	Val	Ile	Val	Ile	Asp	Pro	Ser	Val	Pro	Glu	Asp	
				35					40					45	
Glu	Lys	Ile	Ile	Glu	Gln	Ile	Glu	Asp	Met	Val	Thr	Thr	Ala	Ser	
				50					55					60	
Thr	Tyr	Leu	Phe	Glu	Ala	Thr	Glu	Lys	Arg	Phe	Phe	Phe	Lys	Asn	
				65					70					75	
Val	Ser	Ile	Leu	Ile	Pro	Glu	Asn	Trp	Lys	Glu	Asn	Pro	Gln	Tyr	
				80					85					90	
Lys	Arg	Pro	Lys	His	Glu	Asn	His	Lys	His	Ala	Asp	Val	Ile	Val	
				95					100					105	
Ala	Pro	Pro	Thr	Leu	Pro	Gly	Arg	Asp	Glu	Pro	Tyr	Thr	Lys	Gln	
				110					115					120	
Phe	Thr	Glu	Cys	Gly	Glu	Lys	Gly	Glu	Tyr	Ile	His	Phe	Thr	Pro	
				125					130					135	
Asp	Leu	Leu	Leu	Gly	Lys	Lys	Gln	Asn	Glu	Tyr	Gly	Pro	Pro	Gly	
				140					145					150	
Lys	Leu	Phe	Val	His	Glu	Trp	Ala	His	Leu	Arg	Trp	Gly	Val	Phe	
				155					160					165	
Asp	Glu	Tyr	Asn	Glu	Asp	Gln	Pro	Phe	Tyr	Arg	Ala	Lys	Ser	Lys	
				170					175					180	
Lys	Ile	Glu	Ala	Thr	Arg	Cys	Ser	Ala	Gly	Ile	Ser	Gly	Arg	Asn	
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Arg	Val	Tyr	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Leu	Ser	Arg	Ala	Cys	
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Arg	Ile	Asp	Ser	Thr	Thr	Lys	Leu	Tyr	Gly	Lys	Asp	Cys	Gln	Phe	
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Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met	
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Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His	
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Asn	Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg	
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Ser	Met	Gly	Gly	Lys	Asp	Arg	Leu	Asn	Arg	Met	Asn	Gln	Ala	Ala					
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Lys	His	Phe	Leu	Leu	Gln	Thr	Val	Glu	Asn	Gly	Ser	Trp	Val	Gly					
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Met	Val	His	Phe	Asp	Ser	Thr	Ala	Thr	Ile	Val	Asn	Lys	Leu	Ile					
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Gln	Ile	Lys	Ser	Ser	Asp	Glu	Arg	Asn	Thr	Leu	Met	Ala	Gly	Leu					
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Pro	Thr	Tyr	Pro	Leu	Gly	Gly	Thr	Ser	Ile	Cys	Ser	Gly	Ile	Lys					
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Tyr	Ala	Phe	Gln	Val	Ile	Gly	Glu	Leu	His	Ser	Gln	Leu	Asp	Gly					
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Ser	Glu	Val	Leu	Leu	Leu	Thr	Asp	Gly	Glu	Asp	Asn	Thr	Ala	Ser					
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Ser	Cys	Ile	Asp	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile	Val	His	Phe					
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Thr	Asp	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Leu	Glu	Ser	Lys	Gly	Leu					
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Thr	Leu	Asn	Ser	Asn	Ala	Trp	Met	Asn	Asp	Thr	Val	Ile	Ile	Asp					
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				530					535					540					
Glu	Asn	Phe	Thr	Val	Asp	Ala	Thr	Ser	Lys	Met	Ala	Tyr	Leu	Ser					
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				560					565					570					
Ala	Lys	Ala	Asn	Pro	Glu	Thr	Leu	Thr	Ile	Thr	Val	Thr	Ser	Arg					
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Ala Phe Ile Glu	Ser Gln Asn Gly His	635	Thr Glu Val Leu Glu	640	Leu 645
Leu Asp Asn Gly	Ala Gly Ala Asp Ser	650	Phe Lys Asn Asp Gly	655	Val 660
Tyr Ser Arg Tyr	Phe Thr Ala Tyr Thr	665	Glu Asn Gly Arg Tyr	670	Ser 675
Leu Lys Val Arg	Ala His Gly Gly Ala	680	Asn Thr Ala Arg Leu	685	Lys 690
Leu Arg Pro Pro	Leu Asn Arg Ala Ala	695	Tyr Ile Pro Gly Trp	700	Val 705
Val Asn Gly Glu	Ile Glu Ala Asn Pro	710	Pro Arg Pro Glu Ile	715	Asp 720
Glu Asp Thr Gln	Thr Thr Leu Glu Asp	725	Phe Ser Arg Thr Ala	730	Ser 735
Gly Gly Ala Phe	Val Val Ser Gln Val	740	Pro Ser Leu Pro Leu	745	Pro 750
Asp Gln Tyr Pro	Pro Ser Gln Ile Thr	755	Asp Leu Asp Ala Thr	760	Val 765
His Glu Asp Lys	Ile Ile Leu Thr Trp	770	Thr Ala Pro Gly Asp	775	Asn 780
Phe Asp Val Gly	Lys Val Gln Arg Tyr	785	Ile Ile Arg Ile Ser	790	Ala 795
Ser Ile Leu Asp	Leu Arg Asp Ser Phe	800	Asp Asp Ala Leu Gln	805	Val 810
Asn Thr Thr Asp	Leu Ser Pro Lys Glu	815	Ala Asn Ser Lys Glu	820	Ser 825
Phe Ala Phe Lys	Pro Glu Asn Ile Ser	830	Glu Glu Asn Ala Thr	835	His 840
Ile Phe Ile Ala	Ile Lys Ser Ile Asp	845	Lys Ser Asn Leu Thr	850	Ser 855
Lys Val Ser Asn	Ile Ala Gln Val Thr	860	Leu Phe Ile Pro Gln	865	Ala 870
Asn Pro Asp Asp	Ile Asp Pro Thr Pro	875	Thr Pro Thr Pro Thr	880	Pro 885
Thr Pro Asp Lys	Ser His Asn Ser Gly	890	Val Asn Ile Ser Thr	895	Leu 900
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<210> 380

<211> 3877

<212> DNA

<213> Homo sapiens

<400> 380

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Gly	Val	Lys	Leu	Ala 140	Thr	Glu	Tyr	Ala	Ala 145	Val	Pro	Phe	Asp	Ser 155
Phe	Thr	Leu	Gln	Lys 155	Val	Tyr	Gln	Leu	Glu 160	Thr	Gly	Leu	Thr	Arg 165
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Val	Glu	Ala	Ile	Glu 185	Ser	Ala	Leu	Glu	Thr 190	Leu	Asn	Asn	Pro	Ala 195
Glu	Asn	Ser	Pro	Asn 200	His	Arg	Pro	Tyr	Thr 205	Ala	Ser	Asp	Phe	Ile 210
Glu	Gly	Ile	Tyr	Arg 215	Thr	Glu	Arg	Asp	Lys 220	Gly	Thr	Leu	Tyr	Glu 225
Leu	Thr	Phe	Lys	Gly 230	Asp	His	Lys	His	Glu 235	Phe	Lys	Arg	Leu	Ile 240
Leu	Phe	Arg	Pro	Phe 245	Ser	Pro	Ile	Met	Lys 250	Val	Lys	Asn	Glu	Lys 255
Leu	Asn	Met	Ala	Asn 260	Thr	Leu	Ile	Asn	Val 265	Ile	Val	Pro	Leu	Ala 270
Lys	Arg	Val	Asp	Lys 275	Phe	Arg	Gln	Phe	Met 280	Gln	Asn	Phe	Arg	Glu 285
Met	Cys	Ile	Glu	Gln 290	Asp	Gly	Arg	Val	His 295	Leu	Thr	Val	Val	Tyr 300
Phe	Gly	Lys	Glu	Glu 305	Ile	Asn	Glu	Val	Lys 310	Gly	Ile	Leu	Glu	Asn 315
Thr	Ser	Lys	Ala	Ala 320	Asn	Phe	Arg	Asn	Phe 325	Thr	Phe	Ile	Gln	Leu 330
Asn	Gly	Glu	Phe	Ser 335	Arg	Gly	Lys	Gly	Leu 340	Asp	Val	Gly	Ala	Arg 345
Phe	Trp	Lys	Gly	Ser 350	Asn	Val	Leu	Leu	Phe 355	Phe	Cys	Asp	Val	Asp 360
Ile	Tyr	Phe	Thr	Ser 365	Glu	Phe	Leu	Asn	Thr 370	Cys	Arg	Leu	Asn	Thr 375
Gln	Pro	Gly	Lys	Lys 380	Val	Phe	Tyr	Pro	Val 385	Leu	Phe	Ser	Gln	Tyr 390
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 385

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<210> 386

<211> 1346

<212> DNA

<213> Homo sapiens

<400> 386

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<210> 387

<211> 212

<212> PRT

<213> Homo sapiens

<400> 387

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20 25 30

Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn
35 40 45

Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys
50 55 60

Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys
65 70 75

Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp Pro
80 85 90

Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile
95 100 105

Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
110 115 120

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
125 130 135

Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile
140 145 150

Phe Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly
155 160 165

Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp
170 175 180

Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile Glu Asn Gly
185 190 195

Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly Ile Leu Met Met
200 205 210

Pro Ser

<210> 388

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 388

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<210> 389
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 389
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Thr	Ser	Arg	Val	Leu	Glu	Ala	Val	Asn	Gly	Thr	Asp	Ala	Arg	Leu	
				35					40					45	
Lys	Cys	Thr	Phe	Ser	Ser	Phe	Ala	Pro	Val	Gly	Asp	Ala	Leu	Thr	
				50					55					60	
Val	Thr	Trp	Asn	Phe	Arg	Pro	Leu	Asp	Gly	Gly	Pro	Glu	Gln	Phe	
				65					70					75	
Val	Phe	Tyr	Tyr	His	Ile	Asp	Pro	Phe	Gln	Pro	Met	Ser	Gly	Arg	
				80					85					90	
Phe	Lys	Asp	Arg	Val	Ser	Trp	Asp	Gly	Asn	Pro	Glu	Arg	Tyr	Asp	
				95					100					105	
Ala	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Gln	Phe	Asp	Asp	Asn	Gly	Thr	
				110					115					120	
Tyr	Thr	Cys	Gln	Val	Lys	Asn	Pro	Pro	Asp	Val	Asp	Gly	Val	Ile	
				125					130					135	
Gly	Glu	Ile	Arg	Leu	Ser	Val	Val	His	Thr	Val	Arg	Phe	Ser	Glu	
				140					145					150	
Ile	His	Phe	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Ala	Cys	Ala	Leu	Met	
				155					160					165	
Ile	Ile	Ile	Val	Ile	Val	Val	Val	Leu	Phe	Gln	His	Tyr	Arg	Lys	
				170					175					180	
Lys	Arg	Trp	Ala	Glu	Arg	Ala	His	Lys	Val	Val	Glu	Ile	Lys	Ser	
				185					190					195	
Lys	Glu	Glu	Glu	Arg	Leu	Asn	Gln	Glu	Lys	Lys	Val	Ser	Val	Tyr	
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Leu	Glu	Asp	Thr	Asp											
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<210> 390

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

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<210> 391

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

acaggcagag ccaatggcca gagc 24

<210> 392
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
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<210> 393
<211> 471
<212> DNA
<213> Homo sapiens

<400> 393
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atccgacaac agctgctcca gctgacacgt atccagctac tggctctgct 150
gatgatgaag cccctgatgc tgaaaccact gctgctgcaa ccactgcgac 200
cactgctgct cctaccactg caaccaccgc tgcttctacc actgctcgta 250
aagacattcc agttttaccc aaatggggtg gggatctccc gaatggtaga 300
gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350
tattcatgct tctgtgatt tcatccaact acttaccttg cctacgatat 400
cccctttatc tctaatacagt ttattttctt tcaaataaaa aataactatg 450
agcaacataa aaaaaaaaaa a 471

<210> 394
<211> 90
<212> PRT
<213> Homo sapiens

<400> 394
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe
1 5 10 15
Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr
20 25 30
Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu
35 40 45
Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr
50 55 60
Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val
65 70 75
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
80 85 90

<210> 395
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
gctccctgat cttcatgtca ccacc 25

<210> 396
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
cagggacaca ctctaccatt cgggag 26

<210> 397
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
ccatcttttct ggtctctgcc cagaatccga caacagctgc tc 42

<210> 398
<211> 907
<212> DNA
<213> Homo sapiens

<400> 398
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aaccttggac ccctaggggt ctggatttgc tggtaacaa gataacctga 100
gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150
gtgttcacgg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200
ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250
ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300
gcaggagggg gacagttctg ttgtgcttgg ttggacagta agaggggtctt 350
ggccagtcca ggggtggggg cggcaaactc cataaagaac cagaggggtct 400
gggccccggc cacagagtca tctgccagc tcctctgctg ctggccagtg 450
ggagtggcac gaggtggggc tttgtgccag taaaaccaca ggctggattt 500
gcctgcgggc catggtccct gtctagggca gcaattctca accttcttgc 550
tctcaggacc ccaaagagct ttcatgtat ctattgattt ttaccacatt 600
agcaattaaa actgagaaat gggccgggca cggtggctca cgcctgtaat 650

cccagcactt tgggaggccg aggcgggtgg atcacctgag atcaggagtt 700
 caagaccagc ctggccaaca tgggtgaaacc ttgtctacta aaaatacaaa 750
 aaattagcca ggcacagtgg tgtgcactgg tagtcccagt tactcgggag 800
 gctgaggcag gaaaatcgct tgaacccagg aggcggacgt tgcggtgagc 850
 cgagatcgcg ccgctgattc cagcctgggc gacaagagtg agactccatc 900
 tcacaca 907

<210> 399
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 399
 Met Leu Pro Pro Ala Leu Pro Pro Ala Leu Val Phe Thr Val Ala
 1 5 10 15
 Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu
 20 25 30
 Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly
 35 40 45
 Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg
 50 55 60
 Ala Gly Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg
 65 70 75
 Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn
 80 85 90
 Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu
 95 100 105
 Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln
 110 115 120

<210> 400
 <211> 893
 <212> DNA
 <213> Homo sapiens

<400> 400
 gtcattgccag tgcctgctct gtgcctgctc tgggccctgg caatggtgac 50
 ccggcctgcc tcagcggccc ccatgggcgg ccagaaactg gcacagcatg 100
 aggagctgac cctgctcttc catgggaccc tgcagctggg ccaggccctc 150
 aacggtgtgt acaggaccac ggagggacgg ctgacaaagg ccaggaacag 200
 cctgggtctc tatggcgcga caatagaact cctggggcag gaggtcagcc 250
 ggggccggga tgcagcccag gaacttcggg caagcctgtt ggagactcag 300
 atggaggagg atattctgca gctgcaggca gaggccacag ctgaggtgct 350
 gggggagggtg gccaggcac agaaggtgct acgggacagc gtgcagcggc 400

Leu Pro Ala

<210> 402
 <211> 1915
 <212> DNA
 <213> Homo sapiens

<400> 402
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 tgtaattttgc atcctgggtga tcaccttact cctggaccag accaccagcc 100
 acacatccag attaaaagcc aggaagcaca gcaaacgtcg agtgagagac 150
 aaggatggag atctgaagac tcaaattgaa aagctctgga cagaagtcaa 200
 tgccttgaag gaaattcaag ccctgcagac agtctgtctc cgaggcacta 250
 aagttcacia gaaatgctac cttgcttcag aaggtttgaa gcatttccat 300
 gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350
 gaactccgac gaaatcaacg ccctccaaga ctatggtaaa aggagcctgc 400
 cagggtgtcaa tgacttttgg ctgggcatca atgacatggt cacggaaggc 450
 aagtttggtg acgtcaacgg aatcgctatc tccttcctca actgggaccg 500
 tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550
 cagctcaggg caagtggagt gatgaggcct gtcgcagcag caagagatac 600
 atatgcgagt tcaccatccc taaataggtc tttctccaat gtgtcctcca 650
 agcaagattc atcataactt ataggttcat gatctctaag atcaagtaaa 700
 aatcataatt tttacttatt aaaaaattgc aacacaagat caatgtccat 750
 agcaatatga tagcatcagc caattttgct aacacatttc tttgggattt 800
 tgcccttcct ggggtatagg ggatcagaaa tattgatcca tgtgcacgca 850
 gataaaatgg cttctgctaa acagactaaa atctttctct ctagtctttc 900
 tcacttgtag aaaccagtt tgttttcaaa aaatcacagt agcaatgcaa 950
 ctcatcactc tagaaaagca agcttaggct acctgaaaga ttttcccttg 1000
 gaagtttagc gtatgtttga ctaacaaaaa ttccctacat cagagactct 1050
 aggtgctata taatccaaaa acttttcagc ctgttgctca ttctgtccca 1100
 tgctggcaat aataccttgt cagccatta cccttatatt gaattgctcc 1150
 atctcctggg gggacttgta tcttgtctgc catatcagaa cacaaacccc 1200
 tgaagagggt ctgatttgat tttttttttt tcttcatgcc tacccttttt 1250
 ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatattg 1300

ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400
 ctggagcatc tacacctgag gacaagacgc tgcccacccg cgagggctga 450
 aaaccccgcc ggggggagga ccgtccatcc ccttcccccg gcccctctca 500
 ataacgtgg ttaagagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550
 aaaaaaaaaa aaaaaaaaaa 570

<210> 408
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys
 1 5 10 15
 Ser Ser Ala Ala Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala
 20 25 30
 Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly
 35 40 45
 Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu
 50 55 60
 Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser
 65 70 75
 Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val
 80 85 90
 Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly
 95 100

<210> 409
 <211> 2089
 <212> DNA
 <213> Homo sapiens

<400> 409
 tgaaggactt ttccaggacc caaggccaca cactggaagt cttgcagctg 50
 aagggaggca ctccttggcc tccgcagccg atcacatgaa ggtggtgcca 100
 agtctcctgc tctccgtcct cctggcacag gtgtggttgg taccggctt 150
 ggcccccagt cctcagtgcg cagagacccc agcccoctcag aaccagacca 200
 gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250
 agcgaggaga aggccggtga ggaagagaaa gcctggctga tggccagcag 300
 gcagcagctt gccaaggaga cttcaaactt cggattcagc ctgctgcgaa 350
 agatctccat gaggcacgat ggcaacatgg tcttctctcc atttggcatg 400
 tccttggcca tgacaggctt gatgctgggg gccacagggc cgactgaaac 450
 ccagatcaag agagggctcc acttgaggcc cctgaagccc accaagccc 500

ggctcctgcc ttccctcttt aagggactca gagagaccct ctcccgaac 550
 ctggaactgg gcctctcaca ggggagtttt gccttcatcc acaaggattt 600
 tgatgtcaaa gagactttct tcaatttatc caagaggtat tttgatacag 650
 agtgcgtgcc tatgaatttt cgcaatgcct cacaggccaa aaggctcatg 700
 aatcattaca ttaacaaaga gactcggggg aaaattccca aactgtttga 750
 tgagattaat cctgaaacca aattaattct tgtggattac atcttgttca 800
 aagggaatg gttgacccca tttgaccctg tcttcaccga agtcgacact 850
 ttccacctgg acaagtacaa gaccattaag gtgcccata tgtacggtgc 900
 aggcaagttt gcctccacct ttgacaagaa ttttcgttgt catgtcctca 950
 aactgcccta ccaaggaaat gccaccatgc tgggtggcct catggagaaa 1000
 atgggtgacc acctcgccct tgaagactac ctgaccacag acttgggtga 1050
 gacatggctc agaaacatga aaaccagaaa catggaagtt ttctttccga 1100
 agttcaagct agatcagaag tatgagatgc atgagctgct taggcagatg 1150
 ggaatcagaa gaatcttctc accttttgct gaccttagtg aactctcagc 1200
 tactggaaga aatctccaag tatccagggt tttacgaaga acagtgattg 1250
 aagttgatga aaggggcact gaggcagtg caggaatctt gtcagaaatt 1300
 actgcttatt ccatgcctcc tgtcatcaaa gtggaccggc catttcattt 1350
 catgatctat gaagaaacct ctggaatgct tctgtttctg ggcagggtgg 1400
 tgaatccgac tctcctataa ttcaggacat gcataagcac ttcgtgctgt 1450
 agtagatgct gaatctgagg tatcaaacac acacaggata ccagcaatgg 1500
 atggcagggg agagtgttcc tttgtttctt aactagttta ggggtgttctc 1550
 aaataaatac agtagtcccc acttatctga gggggataca ttcaaagacc 1600
 cccagcagat gcctgaaacg gtggacagtg ctgaacctta tatatatttt 1650
 ttcttacaca tacataccta tgataaagtt taatttataa attaggcaca 1700
 gtaagagatt aacaataata acaacattaa gtaaaatgag ttacttgaac 1750
 gcaagcactg caataccata acagtcaaac tgattataga gaaggctact 1800
 aagtgactca tgggcgagga gcatagacag tgtggagaca ttgggcaagg 1850
 ggagaattca catcctgggt gggacagagc aggacgatgc aagattccat 1900
 cccactactc agaatggcat gctgcttaag acttttagat tgtttatttc 1950
 tggaattttt catttaagt ttttgacca tggttgacca tggttaactg 2000
 agactgcaga aagcaaaacc atggataagg gaggactact acaaaagcat 2050
 taaattgata catatttttt aaaaaaaaaa aaaaaaaaaa 2089

<210> 410
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 410

Met	Lys	Val	Val	Pro	Ser	Leu	Leu	Leu	Ser	Val	Leu	Leu	Ala	Gln
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Val	Trp	Leu	Val	Pro	Gly	Leu	Ala	Pro	Ser	Pro	Gln	Ser	Pro	Glu
				20					25					30
Thr	Pro	Ala	Pro	Gln	Asn	Gln	Thr	Ser	Arg	Val	Val	Gln	Ala	Pro
				35					40					45
Arg	Glu	Glu	Glu	Glu	Asp	Glu	Gln	Glu	Ala	Ser	Glu	Glu	Lys	Ala
				50					55					60
Gly	Glu	Glu	Glu	Lys	Ala	Trp	Leu	Met	Ala	Ser	Arg	Gln	Gln	Leu
				65					70					75
Ala	Lys	Glu	Thr	Ser	Asn	Phe	Gly	Phe	Ser	Leu	Leu	Arg	Lys	Ile
				80					85					90
Ser	Met	Arg	His	Asp	Gly	Asn	Met	Val	Phe	Ser	Pro	Phe	Gly	Met
				95					100					105
Ser	Leu	Ala	Met	Thr	Gly	Leu	Met	Leu	Gly	Ala	Thr	Gly	Pro	Thr
				110					115					120
Glu	Thr	Gln	Ile	Lys	Arg	Gly	Leu	His	Leu	Gln	Ala	Leu	Lys	Pro
				125					130					135
Thr	Lys	Pro	Gly	Leu	Leu	Pro	Ser	Leu	Phe	Lys	Gly	Leu	Arg	Glu
				140					145					150
Thr	Leu	Ser	Arg	Asn	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Gly	Ser	Phe
				155					160					165
Ala	Phe	Ile	His	Lys	Asp	Phe	Asp	Val	Lys	Glu	Thr	Phe	Phe	Asn
				170					175					180
Leu	Ser	Lys	Arg	Tyr	Phe	Asp	Thr	Glu	Cys	Val	Pro	Met	Asn	Phe
				185					190					195
Arg	Asn	Ala	Ser	Gln	Ala	Lys	Arg	Leu	Met	Asn	His	Tyr	Ile	Asn
				200					205					210
Lys	Glu	Thr	Arg	Gly	Lys	Ile	Pro	Lys	Leu	Phe	Asp	Glu	Ile	Asn
				215					220					225
Pro	Glu	Thr	Lys	Leu	Ile	Leu	Val	Asp	Tyr	Ile	Leu	Phe	Lys	Gly
				230					235					240
Lys	Trp	Leu	Thr	Pro	Phe	Asp	Pro	Val	Phe	Thr	Glu	Val	Asp	Thr
				245					250					255
Phe	His	Leu	Asp	Lys	Tyr	Lys	Thr	Ile	Lys	Val	Pro	Met	Met	Tyr
				260					265					270
Gly	Ala	Gly	Lys	Phe	Ala	Ser	Thr	Phe	Asp	Lys	Asn	Phe	Arg	Cys
				275					280					285

His Val Leu Lys	Leu Pro Tyr Gln Gly	Asn Ala Thr Met Leu Val	290	295	300
Val Leu Met Glu	Lys Met Gly Asp His	Leu Ala Leu Glu Asp Tyr	305	310	315
Leu Thr Thr Asp	Leu Val Glu Thr Trp	Leu Arg Asn Met Lys Thr	320	325	330
Arg Asn Met Glu	Val Phe Phe Pro Lys	Phe Lys Leu Asp Gln Lys	335	340	345
Tyr Glu Met His	Glu Leu Leu Arg Gln	Met Gly Ile Arg Arg Ile	350	355	360
Phe Ser Pro Phe	Ala Asp Leu Ser Glu	Leu Ser Ala Thr Gly Arg	365	370	375
Asn Leu Gln Val	Ser Arg Val Leu Arg	Arg Thr Val Ile Glu Val	380	385	390
Asp Glu Arg Gly	Thr Glu Ala Val Ala	Gly Ile Leu Ser Glu Ile	395	400	405
Thr Ala Tyr Ser	Met Pro Pro Val Ile	Lys Val Asp Arg Pro Phe	410	415	420
His Phe Met Ile	Tyr Glu Glu Thr Ser	Gly Met Leu Leu Phe Leu	425	430	435
Gly Arg Val Val	Asn Pro Thr Leu Leu		440		

<210> 411
 <211> 636
 <212> DNA
 <213> Homo sapiens

<400> 411
 ctgggatcag ccaactgcagc tccctgagca ctctctacag agacgcggac 50
 cccagacatg aggaggctcc tccctggtcac cagcctggtg gttgtgctgc 100
 tgtgggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150
 gtcaaactact ggccctcaga gcaggaccca gagaaggcct ggggcgccccg 200
 tgtggtggag cctccggaga aggacgacca gctggtggtg ctgttccctg 250
 tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300
 aggggccccca tccttccagg caccaaggcc tggatggaga ccgaggacac 350
 cctggggccgt gtccctgagtc ccgagcccga ccatgacagc ctgtaccacc 400
 ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450
 ccaaatacacc aggtgctcct gggaccggag gaagaccaag accacatcta 500
 ccacccccag tagggctcca ggggccatca ctgccccgc cctgtcccaa 550
 ggcccaggct gttgggactg ggaccctccc taccctgccc cagctagaca 600

aataaaccccc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412
<211> 151
<212> PRT
<213> Homo sapiens

<400> 412
Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu
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Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met
20 25 30
Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp
35 40 45
Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val
50 55 60
Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu
65 70 75
Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys
80 85 90
Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro
95 100 105
Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp
110 115 120
Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln
125 130 135
Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro
140 145 150
Gln

<210> 413
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 413
agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga 50
aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150
tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200
gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250
gtgcatttga tggcctgtat tttctccgca ctgagaatgg tgttatctac 300
cagaccttct gtgacatgac ctctgggggt ggcggtgga ccctggtggc 350
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcatcgct 400

ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450
 tgggccaaact acaacacctt tggatctgca gaggcggcca cgagcgatga 500
 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550
 ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600
 ctgaggtacc gcacggacac tggcttcctc cagacactgg gacataatct 650
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 gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850
 tgtgtgctgg aatgaggggtc accggatgta aactgagca tcaactgcatt 900
 ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt 950
 ttctggtttt gattggagtg gatatggaac tcatgttggt tacagcagca 1000
 gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050
 tgtgggaggg aaccagacc tctcctcca accatgagat cccaaggatg 1100
 gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150
 taaatcatat tgactcaaga aaaaaa 1176

<210> 414
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg
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 Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr
 20 25 30
 Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys
 35 40 45
 Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr
 50 55 60
 Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly
 65 70 75
 Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met
 80 85 90
 Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly
 95 100 105
 Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr
 110 115 120
 Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys

125										130					135				
Asn	Pro	Gly	Tyr	Tyr	Asp	Ile	Gln	Ala	Lys	Asp	Leu	Gly	Ile	Trp					
				140					145					150					
His	Val	Pro	Asn	Lys	Ser	Pro	Met	Gln	His	Trp	Arg	Asn	Ser	Ser					
				155					160					165					
Leu	Leu	Arg	Tyr	Arg	Thr	Asp	Thr	Gly	Phe	Leu	Gln	Thr	Leu	Gly					
				170					175					180					
His	Asn	Leu	Phe	Gly	Ile	Tyr	Gln	Lys	Tyr	Pro	Val	Lys	Tyr	Gly					
				185					190					195					
Glu	Gly	Lys	Cys	Trp	Thr	Asp	Asn	Gly	Pro	Val	Ile	Pro	Val	Val					
				200					205					210					
Tyr	Asp	Phe	Gly	Asp	Ala	Gln	Lys	Thr	Ala	Ser	Tyr	Tyr	Ser	Pro					
				215					220					225					
Tyr	Gly	Gln	Arg	Glu	Phe	Thr	Ala	Gly	Phe	Val	Gln	Phe	Arg	Val					
				230					235					240					
Phe	Asn	Asn	Glu	Arg	Ala	Ala	Asn	Ala	Leu	Cys	Ala	Gly	Met	Arg					
				245					250					255					
Val	Thr	Gly	Cys	Asn	Thr	Glu	His	His	Cys	Ile	Gly	Gly	Gly	Gly					
				260					265					270					
Tyr	Phe	Pro	Glu	Ala	Ser	Pro	Gln	Gln	Cys	Gly	Asp	Phe	Ser	Gly					
				275					280					285					
Phe	Asp	Trp	Ser	Gly	Tyr	Gly	Thr	His	Val	Gly	Tyr	Ser	Ser	Ser					
				290					295					300					
Arg	Glu	Ile	Thr	Glu	Ala	Ala	Val	Leu	Leu	Phe	Tyr	Arg							
				305					310										

<210> 415
 <211> 1281
 <212> DNA
 <213> Homo sapiens

<400> 415
 gcggagccgg cgccggctgc gcagaggagc cgctctcgcc gccgccacct 50
 cggtggggag cccacgaggc tgccgcatcc tgccctcgga acaatgggac 100
 tcggcgcgcg aggtgcttgg gcgcgctgc tcctggggac gctgcaggtg 150
 ctacgctgc tgggggcccgc ccatgaaagc gcagccatgg cggcatctgc 200
 aaacatagag aattctgggc ttccacacaa ctccagtgt aactcaacag 250
 agactotcca acatgtgcct tctgaccata caaatgaaac ttccaacagt 300
 actgtgaaac caccaacttc agttgcctca gactccagta atacaacggt 350
 caccaccatg aaacctacag cggcatctaa tacaacaaca ccagggatgg 400
 tctcaacaaa tatgacttct accacottaa agtctacacc caaaacaaca 450
 agtgtttcac agaacacatc tcagatatca acatccacaa tgaccgtaac 500

<p> 1. <i>Staphylococcus aureus</i> (n=10) 2. <i>Staphylococcus aureus</i> (n=10) 3. <i>Staphylococcus aureus</i> (n=10) 4. <i>Staphylococcus aureus</i> (n=10) 5. <i>Staphylococcus aureus</i> (n=10) 6. <i>Staphylococcus aureus</i> (n=10) 7. <i>Staphylococcus aureus</i> (n=10) 8. <i>Staphylococcus aureus</i> (n=10) 9. <i>Staphylococcus aureus</i> (n=10) 10. <i>Staphylococcus aureus</i> (n=10) </p>	
1	100
2	100
3	100
4	100
5	100
6	100
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34	100
35	100
36	100
37	100
38	100
39	100
40	100
41	100
42	100
43	100
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cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgagc ctgtcagacg 200
ccgccaagaa ttctgaggat gtcagatgta aatgtatctg ccctccctat 250
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tgattgcctt catgtttgtg agcccatgcc tgtgcggggg cctgatgtag 350
aagcatactg tctacgctgt gaatgcaa atgaagaaag aagctctgtc 400
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 Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile
 35 40 45
 Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn
 50 55 60
 Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu Pro Met
 65 70 75
 Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu
 80 85 90
 Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
 95 100 105
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val
 110 115 120
 Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly
 125 130 135

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Pro	Phe	Ala	Asn	Ala	His	Asp	Val	Leu	Ala	Arg	Ser	Arg	Ser	Arg
				155					160					165
Ala	Asn	Val	Leu	Asn	Lys	Val	Glu	Tyr	Ala	Gln	Gln	Arg	Trp	Lys
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 ctgcctctc ttcatgaggt acttaggata gccattatct cagtttcaca 550
 taagaatgtt tactcaatgt ttaagtgttt tgccccaaaa ttcacaacta 600
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 35 40 45

Arg Phe Pro Pro Met Met His His His Gln Ala Pro Ser Asp Gly
50 55 60
Gln Thr Pro Gly Ala Arg Phe Gln Arg Ser His Leu Ala Glu Ala
65 70 75
Phe Ala Lys Ala Lys Gly Ser Gly Gly Gly Ala Gly Gly Gly Gly
80 85 90
Ser Gly Arg Gly Leu Met Gly Gln Ile Ile Pro Ile Tyr Gly Phe
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Gly Ile Phe Leu Tyr Ile Leu Tyr Ile Leu Phe Lys Val Ser Arg
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Ile Ile Leu Ile Ile Leu His Gln
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 35 40 45
 Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn
 50 55 60
 Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln
 65 70 75
 Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser Glu Leu
 80 85 90
 Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr Asn
 95 100 105
 Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn
 110 115 120
 Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala

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Ala Arg Thr His	Leu Ile Arg Trp Val	Gly Leu Ser Arg Gln	Lys		
	155	160	165		
Ser Asn Glu Val	Trp Lys Trp Glu Asp	Gly Ser Val Ile Ser	Glu		
	170	175	180		
Asn Met Phe Glu	Phe Leu Glu Asp Gly	Lys Gly Asn Met Asn	Cys		
	185	190	195		
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 <210> 471
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 <210> 490
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 <223> Synthetic oligonucleotide probe

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 gctcagccaa acactgtca 19

 <210> 491
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 491
 ggggccctga cagtgtt 17

[illegible]

<400> 494					
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cagcccgcgc	gggagccgga	ccgccgccgg	aggagctcgg	acggcatgct	150
gagccccctc	ctttgctgaa	gcccgagtcg	ggagaagccc	gggcaaacgc	200
aggctaagga	gaccaaagcg	gcgaagtcgc	gagacagcgg	acaagcagcg	250
gaggagaagg	aggaggaggc	gaaccacagag	aggggcagca	aaagaagcgg	300
tggttggtggg	cgtcgtggcc	atggcgggcg	ctatcgccag	ctcgctcatc	350
cgtcagaaga	ggcaagcccg	cgagcgcgag	aaatccaacg	cctgcaagtg	400
tgtcagcagc	cccagcaaag	gcaagaccag	ctgcgacaaa	aacaagttaa	450
atgtcttttc	ccgggtcaaa	ctcttcggct	ccaagaagag	gcgcagaaga	500
agaccagagc	ctcagcttaa	gggtatagtt	accaagctat	acagccgaca	550
aggctaccac	ttgcagctgc	aggcggatgg	aaccattgat	ggcaccaaag	600
atgaggacag	cacttacact	ctgtttaacc	tcattccctgt	gggtctgcga	650
gtggtggcta	tccaaggagt	tcaaaccaag	ctgtacttgg	caatgaacag	700
tgagggatac	ttgtacacct	cggaaactttt	cacacctgag	tgcaaattca	750
aagaatcagt	gtttgaaaat	tattatgtga	catattcatc	aatgatatac	800
cgtcagcagc	agtcaggccg	agggtggtat	ctgggtctga	acaaagaagg	850
aqagatcatg	aaaggcaacc	atgtgaagaa	gaacaagcct	gcagctcatt	900

[illegible]

<400> 495

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  1             5             10             15
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Ser Arg Ser Val	Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser				
	230		235		240
His Asn Glu Ser Thr					
	245				

<210> 496
 <211> 1471
 <212> DNA
 <213> Homo Sapien

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 gagccctgtc ttactgaacc tgggcaacct ggatattctg agacatatatt 150
 tgggggggatt tcagtgaaaa aagtggggga tcccctccat ttagagtgtg 200
 gcaaaggaaa aaacaccaag gttgggttcc ttctgacat tggcagtgcc 250
 ccagtagggg tgggatgagc gaatattccc aaagctaaag tcccacaccc 300
 tgtagattac aagagtggat ttggcaggag tgtgccccaa aatacagtgg 350
 aaaggtgcct gaagatatatt aaaccacgtc ttggaaaattt agtgggtctt 400
 ggctttggga taggtgaagt gaggacagac actggagagg agggaaaggg 450
 gacgttttca ataggaggca aaactcgagg gtgggatcca ctgaggagta 500
 cataggctgc tggatctggt ggagccagca ctggggccac ggggtggtaac 550
 tggctgtctg ggaggggggt acgtgagggg ggggtctggg gcttatcctc 600
 aggtcctgtg ggtggggcag cgagtcgggg cctgagcgtc aagagcatgc 650
 cctagtgagc gggctcctct gggggagccc agcgcgctcc gggcgctgc 700
 cggtttgggg gtgtctcctc ccggggcgct atggcggcgc tggccagtag 750
 cctgatccgg cagaagcggg aggtccgcga gcccgggggc agccggccgg 800
 tgtcggcgca gcggcgctg tgtccccgcg gcaccaagtc cctttgccag 850
 aagcagctcc tcacctctgt gtccaagggt cgactgtgcg gggggcggcc 900
 cgcgcgggcg gaccgcggcc cggagcctca gctcaaaggc atcgtcacca 950
 aactgttctg ccgccagggt ttctacctcc aggcgaatcc cgacggaagc 1000
 atccagggca cccagagga taccagctcc ttcacccact tcaacctgat 1050
 ccctgtgggc ctccgtgtgg tcaccatcca gagcgccaag ctgggtcact 1100
 acatggccat gaatgctgag ggactgctct acagttcgcc gcatttcaca 1150
 gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtcctgta 1200
 cgcctctgct ctctaccgcc agcgtcgttc tggccggggc tggtagctcg 1250

gcctggacaa ggagggccag gtcataagg gaaaccgagt taagaagacc 1300
aaggcagctg cccactttct gcccaagctc ctggaggtgg ccatgtacca 1350
ggagccttct ctccacagtg tccccgaggc ctcccccttc agtccccctg 1400
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ccagccacca ccacaacctg t 1471

<210> 497
<211> 225
<212> PRT
<213> Homo Sapien

<400> 497
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Cys Pro Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile
35 40 45
Leu Leu Ser Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro
50 55 60
Asp Arg Gly Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu
65 70 75
Phe Cys Arg Gln Gly Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser
80 85 90
Ile Gln Gly Thr Pro Glu Asp Thr Ser Ser Phe Thr His Phe Asn
95 100 105
Leu Ile Pro Val Gly Leu Arg Val Val Thr Ile Gln Ser Ala Lys
110 115 120
Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly Leu Leu Tyr Ser
125 130 135
Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu Cys Val Phe
140 145 150
Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg Gln Arg
155 160 165
Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly Gln
170 175 180
Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala Ala Ala His
185 190 195
Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser
200 205 210
Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro
215 220 225

<210> 498
<211> 744

<212> DNA
<213> Homo Sapien

<400> 498

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gcaagaaccg cgggctctgc aacggcaacc tgggtggatat cttctccaaa 150
gtgcgcacatc tgggcctcaa gaagcgcagg ttgcggcgcc aagatcccca 200
gctcaagggg atagtgaaca gggtatattg caggcaaggc tactacttgc 250
aaatgcaccc cgatggagct ctcatggaa ccaaggatga cagcactaat 300
tctacactct tcaacctcat accagtggga ctacgtgttg ttgccatcca 350
gggagtgaaa acagggttgt atatagccat gaatggagaa ggttacctct 400
acccatcaga actttttacc cctgaatgca agtttaaaga atctgttttt 450
gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500
tggtagagcc tgggtttttg gattaaataa ggaagggcaa gctatgaaag 550
ggaacagagt aaagaaaacc aaaccagcag ctcattttct acccaagcca 600
ttggaagtgt ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650
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<210> 499

<211> 247

<212> PRT

<213> Homo Sapien

<400> 499

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Ala	Arg	Glu	Gln	His	Trp	Asp	Arg	Pro	Ser	Ala	Ser	Arg	Arg	Arg
				20					25					30
Ser	Ser	Pro	Ser	Lys	Asn	Arg	Gly	Leu	Cys	Asn	Gly	Asn	Leu	Val
				35					40					45
Asp	Ile	Phe	Ser	Lys	Val	Arg	Ile	Phe	Gly	Leu	Lys	Lys	Arg	Arg
				50					55					60
Leu	Arg	Arg	Gln	Asp	Pro	Gln	Leu	Lys	Gly	Ile	Val	Thr	Arg	Leu
				65					70					75
Tyr	Cys	Arg	Gln	Gly	Tyr	Tyr	Leu	Gln	Met	His	Pro	Asp	Gly	Ala
				80					85					90
Leu	Asp	Gly	Thr	Lys	Asp	Asp	Ser	Thr	Asn	Ser	Thr	Leu	Phe	Asn
				95					100					105
Leu	Ile	Pro	Val	Gly	Leu	Arg	Val	Val	Ala	Ile	Gln	Gly	Val	Lys
				110					115					120

Thr	Gly	Leu	Tyr	Ile	Ala	Met	Asn	Gly	Glu	Gly	Tyr	Leu	Tyr	Pro
				125					130					135
Ser	Glu	Leu	Phe	Thr	Pro	Glu	Cys	Lys	Phe	Lys	Glu	Ser	Val	Phe
				140					145					150
Glu	Asn	Tyr	Tyr	Val	Ile	Tyr	Ser	Ser	Met	Leu	Tyr	Arg	Gln	Gln
				155					160					165
Glu	Ser	Gly	Arg	Ala	Trp	Phe	Leu	Gly	Leu	Asn	Lys	Glu	Gly	Gln
				170					175					180
Ala	Met	Lys	Gly	Asn	Arg	Val	Lys	Lys	Thr	Lys	Pro	Ala	Ala	His
				185					190					195
Phe	Leu	Pro	Lys	Pro	Leu	Glu	Val	Ala	Met	Tyr	Arg	Glu	Pro	Ser
				200					205					210
Leu	His	Asp	Val	Gly	Glu	Thr	Val	Pro	Lys	Pro	Gly	Val	Thr	Pro
				215					220					225
Ser	Lys	Ser	Thr	Ser	Ala	Ser	Ala	Ile	Met	Asn	Gly	Gly	Lys	Pro
				230					235					240
Val	Asn	Lys	Ser	Lys	Thr	Thr								
				245										

<210> 500
 <211> 2906
 <212> DNA
 <213> Homo Sapien

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 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
 acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
 ttggtgtgtt ctgacataaa taaataatct taaagcagct gttcccctcc 300
 ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
 gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
 ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgog 550
 gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
 tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650
 ttcacaaacc tccttttttt taaattttta ttccttttgg tatcaagatc 700
 atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800
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 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850
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<210> 501
 <211> 640
 <212> PRT
 <213> Homo Sapien

<400> 501
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 35 40 45
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
 50 55 60
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
 65 70 75
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
 80 85 90
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
 95 100 105
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
 110 115 120
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
 125 130 135
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
 140 145 150
 Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
 155 160 165

Val	Val	Asp	Trp	Glu	Thr	Thr	Asn	Val	Thr	Thr	Ser	Leu	Thr	Pro
				485					490					495
Gln	Ser	Thr	Arg	Ser	Thr	Glu	Lys	Thr	Phe	Thr	Ile	Pro	Val	Thr
				500					505					510
Asp	Ile	Asn	Ser	Gly	Ile	Pro	Gly	Ile	Asp	Glu	Val	Met	Lys	Thr
				515					520					525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Leu	Met	Ala
				530					535					540
Ala	Val	Met	Leu	Val	Ile	Phe	Tyr	Lys	Met	Arg	Lys	Gln	His	His
				545					550					555
Arg	Gln	Asn	His	His	Ala	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn
				560					565					570
Val	Asp	Asp	Glu	Ile	Thr	Gly	Asp	Thr	Pro	Met	Glu	Ser	His	Leu
				575					580					585
Pro	Met	Pro	Ala	Ile	Glu	His	Glu	His	Leu	Asn	His	Tyr	Asn	Ser
				590					595					600
Tyr	Lys	Ser	Pro	Phe	Asn	His	Thr	Thr	Thr	Val	Asn	Thr	Ile	Asn
				605					610					615
Ser	Ile	His	Ser	Ser	Val	His	Glu	Pro	Leu	Leu	Ile	Arg	Met	Asn
				620					625					630
Ser	Lys	Asp	Asn	Val	Gln	Glu	Thr	Gln	Ile					
				635					640					

<210> 502
 <211> 2458
 <212> DNA
 <213> Homo Sapien

<400> 502
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 agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200
 ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250
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 ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450
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 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100
 cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150
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Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr	Gly
	230	235	240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu	Leu
	245	250	255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg	Pro
	260	265	270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu	Val
	275	280	285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser	Gly
	290	295	300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser	Gln
	305	310	315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala	Thr
	320	325	330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu	Pro
	335	340	345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr	Pro
	350	355	360
Ser Met Ile Pro	Ser Gln Ser Arg Ala	Phe Gln Thr Val	
	365	370	

<210> 504
 <211> 3060
 <212> DNA
 <213> Homo Sapien

<400> 504
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 ctctgtgctg gagtagtgga tttcgccaga agtttgagta tcactactcc 150
 tgaagagatg attgaaaaag ccaaagggga aactgcctat ctgccatgca 200
 aatttacgct tagtcccgaa gaccaggac cgctggacat cgagtggctg 250
 atatcaccag ctgataatca gaagtggtat caagtgatta ttttatattc 300
 tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350
 attttacgag taatgatctc aaatctggtg atgcatcaat aaatgtaacg 400
 aatttacaac tgtcagatat tggcacatat cagtgcaaag tgaaaaaagc 450
 tcttggtggt gcaaataaga agattcatct ggtagttctt gttaagcctt 500
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<210> 505

<211> 352

<212> PRT

<213> Homo Sapien

<400> 505

Met	Ala	Leu	Leu	Leu	Cys	Phe	Val	Leu	Leu	Cys	Gly	Val	Val	Asp
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Phe	Ala	Arg	Ser	Leu	Ser	Ile	Thr	Thr	Pro	Glu	Glu	Met	Ile	Glu
				20					25					30

Lys	Ala	Lys	Gly	Glu	Thr	Ala	Tyr	Leu	Pro	Cys	Lys	Phe	Thr	Leu
				35					40					45

Ser	Pro	Glu	Asp	Gln	Gly	Pro	Leu	Asp	Ile	Glu	Trp	Leu	Ile	Ser
				50					55					60

Pro	Ala	Asp	Asn	Gln	Lys	Val	Asp	Gln	Val	Ile	Ile	Leu	Tyr	Ser
				65					70					75

Gly	Asp	Lys	Ile	Tyr	Asp	Asp	Tyr	Tyr	Pro	Asp	Leu	Lys	Gly	Arg
				80					85					90

Val	His	Phe	Thr	Ser	Asn	Asp	Leu	Lys	Ser	Gly	Asp	Ala	Ser	Ile
				95					100					105

Asn	Val	Thr	Asn	Leu	Gln	Leu	Ser	Asp	Ile	Gly	Thr	Tyr	Gln	Cys
				110					115					120

Lys	Val	Lys	Lys	Ala	Pro	Gly	Val	Ala	Asn	Lys	Lys	Ile	His	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

125	130	135
Val Val Leu Val Lys Pro Ser Gly Ala	Arg Cys Tyr Val Asp Gly	
140	145	150
Ser Glu Glu Ile Gly Ser Asp Phe Lys	Ile Lys Cys Glu Pro Lys	
155	160	165
Glu Gly Ser Leu Pro Leu Gln Tyr Glu	Trp Gln Lys Leu Ser Asp	
170	175	180
Ser Gln Lys Met Pro Thr Ser Trp Leu	Ala Glu Met Thr Ser Ser	
185	190	195
Val Ile Ser Val Lys Asn Ala Ser Ser	Glu Tyr Ser Gly Thr Tyr	
200	205	210
Ser Cys Thr Val Arg Asn Arg Val Gly	Ser Asp Gln Cys Leu Leu	
215	220	225
Arg Leu Asn Val Val Pro Pro Ser Asn	Lys Ala Gly Leu Ile Ala	
230	235	240
Gly Ala Ile Ile Gly Thr Leu Leu Ala	Leu Ala Leu Ile Gly Leu	
245	250	255
Ile Ile Phe Cys Cys Arg Lys Lys Arg	Arg Glu Glu Lys Tyr Glu	
260	265	270
Lys Glu Val His His Asp Ile Arg Glu	Asp Val Pro Pro Pro Lys	
275	280	285
Ser Arg Thr Ser Thr Ala Arg Ser Tyr	Ile Gly Ser Asn His Ser	
290	295	300
Ser Leu Gly Ser Met Ser Pro Ser Asn	Met Glu Gly Tyr Ser Lys	
305	310	315
Thr Gln Tyr Asn Gln Val Pro Ser Glu	Asp Phe Glu Arg Thr Pro	
320	325	330
Gln Ser Pro Thr Leu Pro Pro Ala Lys	Phe Lys Tyr Pro Tyr Lys	
335	340	345
Thr Asp Gly Ile Thr Val Val		
350		

<210> 506
 <211> 1705
 <212> DNA
 <213> Homo Sapien

<400> 506
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 ccagctgcct ccaggcagcc agccctcaag catcacttac aggaccagag 150
 ggacaagaca tgactgtgat gaggagctgc ttctcgccaat ttaacaccaa 200
 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaatTT tcaacagagg ctgcaaagcc tgtggactTT agccagaccc 300
 ttctgcccTc ctttgctggc gacagcctct caaatgcaga tggttgtgct 350
 cccttgccTg ggTTTTaccc tgcTTctctg gagccaggta tcagggggccc 400
 agggccaaga attccactTT gggccctgcc aagtgaaggg ggttgttccc 450
 cagaaactgt gggaagcctt ctgggctgtg aaagacacta tgcaagctca 500
 ggataacatc acgagtgcc ggctgctgca gcaggaggTT ctgcagaacg 550
 tctcggatgc tgagagctgt taccttgtcc acaccctgct ggagttctac 600
 ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtcaggac 650
 tctgaagtca ttctctactc tggccaacaa ctttgttctc atcgtgtcac 700
 aactgcaacc cagtcaagaa aatgagatgt tttccatcag agacagtgca 750
 cacaggcggT ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800
 agcagctctg accaaagccc ttggggaagt ggacattctt ctgacctgga 850
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 tgttactgTg acacttcacg cccttggcca tgggtcccat tcttggccca 1000
 ggattattgt caaagaagtc attctttaag cagcgccagt gacagtcagg 1050
 gaaggtgcct ctggatgctg tgaagagtct acagagaaga ttcttgtatt 1100
 tattacaact ctattttaatt aatgtcagta tttcaactga agttctatTT 1150
 atttgtgaga ctgtaagtta catgaaggca gcagaatatt gtgccccatg 1200
 cttctttacc cctcacaatc cttgccacag tgtggggcag tggatgggtg 1250
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 ccctgctaatt aaaagacaac ataactccaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaa 1705

<210> 507
 <211> 206
 <212> PRT

<213> Homo Sapien

<400> 507

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Pro Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met
20 25 30
Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
35 40 45
Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
50 55 60
Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
65 70 75
Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg
80 85 90
Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser
95 100 105
Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val
110 115 120
Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
125 130 135
Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
140 145 150
Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser
155 160 165
Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu
170 175 180
Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile
185 190 195
Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
200 205

<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

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cggctctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150
gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaa 200
gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250
tgtgtgctgc gtgaccaaga acctctggc gttctacgtg gacagggtgt 300

165

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<210> 510
<211> 996
<212> DNA
<213> Homo Sapien
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cacatacgat	ttaggtgaca	ctatagaata	acatccactt	tgcctttctc	150
tccacaggtg	tccactccca	ggtccaactg	cacctcggtt	ctatcgataa	200
tctcagcacc	agccactcag	agcagggcac	gatgttgggg	gcccgcctca	250
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gcctatccca	atgcctcccc	actgctcggc	tccagctggg	gtggcctgat	350
ccacctgtac	acagccacag	ccaggaacag	ctaccacctg	cagatccaca	400
agaatggcca	tgtggatggc	gcaccccatc	agaccatcta	cagtgccttg	450
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ccacggcggc	acacccggag	cgccgaggac	gactcggagc	gggaccccct	800
gaacgtgctg	aagccccggg	cccggatgac	cccggccccg	gcctcctgtt	850
cacaggagct	cccgagcgcc	gaggacaaca	gcccgatggc	cagtgacca	900
ttaggggtgg	tcaggggcgg	tcgagtgaac	acgcacgctg	ggggaacggg	950
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<210> 511
<211> 251
<212> PRT
<213> Homo Sapien
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<400> 511
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   1                                10                      15

Val  Cys  Ser  Met  Ser  Val  Leu  Arg  Ala  Tyr  Pro  Asn  Ala  Ser  Pro
                   20                      25                      30

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Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala
 35 40 45
 Thr Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His
 50 55 60
 Val Asp Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile
 65 70 75
 Arg Ser Glu Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser
 80 85 90
 Arg Arg Tyr Leu Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser
 95 100 105
 His Tyr Phe Asp Pro Glu Asn Cys Arg Phe Gln His Gln Thr Leu
 110 115 120
 Glu Asn Gly Tyr Asp Val Tyr His Ser Pro Gln Tyr His Phe Leu
 125 130 135
 Val Ser Leu Gly Arg Ala Lys Arg Ala Phe Leu Pro Gly Met Asn
 140 145 150
 Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg Arg Asn Glu Ile Pro
 155 160 165
 Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg His Thr Arg Ser
 170 175 180
 Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val Leu Lys Pro
 185 190 195
 Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln Glu Leu
 200 205 210
 Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu Gly
 215 220 225
 Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 230 235 240
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 245 250

<210> 512
 <211> 2015
 <212> DNA
 <213> Homo Sapien

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 ctgctgggag gttggggtct ctgggagctc tgcaggcccc agcaccgcga 150
 gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200
 ctagcaccgg gccacgccgc tctggaaact caaacgctga gcgctgagac 250
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gggtgtccttg gactcacctt ggcacatggt ctgtgtttca gtaaagagag 1950
 acctgatcac ccattctgtgt gcttccatcc tgcattaaaa ttacttcagt 2000
 gtggcccaaa aaaaa 2015

<210> 513
 <211> 482
 <212> PRT
 <213> Homo Sapien

<400> 513

Met	Gly	Cys	Leu	Trp	Gly	Leu	Ala	Leu	Pro	Leu	Phe	Phe	Phe	Cys	1	5	10	15
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Arg	Ala	Asp	Thr	Ala	Met	Thr	Thr	Asp	Asp	Thr	Glu	Val	Pro	Ala	35	40	45	
Met	Thr	Leu	Ala	Pro	Gly	His	Ala	Ala	Leu	Glu	Thr	Gln	Thr	Leu	50	55	60	
Ser	Ala	Glu	Thr	Ser	Ser	Arg	Ala	Ser	Thr	Pro	Ala	Gly	Pro	Ile	65	70	75	
Pro	Glu	Ala	Glu	Thr	Arg	Gly	Ala	Lys	Arg	Ile	Ser	Pro	Ala	Arg	80	85	90	
Glu	Thr	Arg	Ser	Phe	Thr	Lys	Thr	Ser	Pro	Asn	Phe	Met	Val	Leu	95	100	105	
Ile	Ala	Thr	Ser	Val	Glu	Thr	Ser	Ala	Ala	Ser	Gly	Ser	Pro	Glu	110	115	120	
Gly	Ala	Gly	Met	Thr	Thr	Val	Gln	Thr	Ile	Thr	Gly	Ser	Asp	Pro	125	130	135	
Glu	Glu	Ala	Ile	Phe	Asp	Thr	Leu	Cys	Thr	Asp	Asp	Ser	Ser	Glu	140	145	150	
Glu	Ala	Lys	Thr	Leu	Thr	Met	Asp	Ile	Leu	Thr	Leu	Ala	His	Thr	155	160	165	
Ser	Thr	Glu	Ala	Lys	Gly	Leu	Ser	Ser	Glu	Ser	Ser	Ala	Ser	Ser	170	175	180	
Asp	Gly	Pro	His	Pro	Val	Ile	Thr	Pro	Ser	Arg	Ala	Ser	Glu	Ser	185	190	195	
Ser	Ala	Ser	Ser	Asp	Gly	Pro	His	Pro	Val	Ile	Thr	Pro	Ser	Arg	200	205	210	
Ala	Ser	Glu	Ser	Ser	Ala	Ser	Ser	Asp	Gly	Pro	His	Pro	Val	Ile	215	220	225	
Thr	Pro	Ser	Trp	Ser	Pro	Gly	Ser	Asp	Val	Thr	Leu	Leu	Ala	Glu	230	235	240	
Ala	Leu	Val	Thr	Val	Thr	Asn	Ile	Glu	Val	Ile	Asn	Cys	Ser	Ile	245	250	255	

Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp	260	265	270
Ile	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	275	280	285
Asp	Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	290	295	300
Thr	Glu	Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	305	310	315
Thr	Glu	Ser	Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	320	325	330
Thr	Asn	Ser	Ala	Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	335	340	345
Thr	Leu	Ser	Gly	Ala	Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	350	355	360
Glu	Thr	Ser	Ala	Leu	Ser	Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	365	370	375
Ser	Gly	Ala	Ala	Pro	Val	Ser	Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly	380	385	390
Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser	Ser	Ala	Ser	Ser	Tyr	Ser	Pro	395	400	405
Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr	Pro	Ser	Glu	Thr	Pro	Thr	410	415	420
Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro	Thr	Ser	Arg	Asp	Pro	425	430	435
Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser	Ser	Arg	Gly	Thr	440	445	450
Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys	Thr	Thr	Met	455	460	465
Lys	Pro	Gln	Gln	Pro	Arg	Pro	Arg	Leu	Pro	Gly	Arg	Gly	Arg	Pro	470	475	480

Gln Thr

<210> 514
 <211> 2284
 <212> DNA
 <213> Homo Sapien

<400> 514
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 ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150
 cttcttaaag caaactaaga ccagaggagg gattatcctt gacctttgaa 200
 gacccaaaact aaactgaaat ttaaaatggt cttcggggga gaaggagct 250

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<210> 515

<211> 431

<212> PRT

<213> Homo Sapien

<400> 515

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Ile	Cys	Phe	Leu	Thr	Leu	Arg	Leu	Ser	Ala	Ser	Gln	Asn	Cys	Leu
				20					25					30
Lys	Lys	Ser	Leu	Glu	Asp	Val	Val	Ile	Asp	Ile	Gln	Ser	Ser	Leu
				35					40					45
Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln
				50					55					60
Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly
				65					70					75
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala
				80					85					90
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala
				95					100					105
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile
				110					115					120
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu
				125					130					135
Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val
				140					145					150
Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp
				155					160					165
Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp
				170					175					180
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu
				185					190					195

Leu	Ala	Tyr	Lys	Glu	Lys	Gly	His	Ser	Gln	Ser	Ser	Gln	Phe	Ser	
				200					205					210	
Ser	Asp	Gln	Glu	Ile	Ala	His	Leu	Leu	Pro	Glu	Asn	Val	Ser	Ala	
				215					220					225	
Leu	Pro	Ala	Thr	Val	Ala	Val	Ala	Ser	Pro	His	Thr	Thr	Ser	Ala	
				230					235					240	
Thr	Pro	Lys	Pro	Ala	Thr	Leu	Leu	Pro	Thr	Asn	Ala	Ser	Val	Thr	
				245					250					255	
Pro	Ser	Gly	Thr	Ser	Gln	Pro	Gln	Leu	Ala	Thr	Thr	Ala	Pro	Pro	
				260					265					270	
Val	Thr	Thr	Val	Thr	Ser	Gln	Pro	Pro	Thr	Thr	Leu	Ile	Ser	Thr	
				275					280					285	
Val	Phe	Thr	Arg	Ala	Ala	Ala	Thr	Leu	Gln	Ala	Met	Ala	Thr	Thr	
				290					295					300	
Ala	Val	Leu	Thr	Thr	Thr	Phe	Gln	Ala	Pro	Thr	Asp	Ser	Lys	Gly	
				305					310					315	
Ser	Leu	Glu	Thr	Ile	Pro	Phe	Thr	Glu	Ile	Ser	Asn	Leu	Thr	Leu	
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Asn	Thr	Gly	Asn	Val	Tyr	Asn	Pro	Thr	Ala	Leu	Ser	Met	Ser	Asn	
				335					340					345	
Val	Glu	Ser	Ser	Thr	Met	Asn	Lys	Thr	Ala	Ser	Trp	Glu	Gly	Arg	
				350					355					360	
Glu	Ala	Ser	Pro	Gly	Ser	Ser	Ser	Gln	Gly	Ser	Val	Pro	Glu	Asn	
				365					370					375	
Gln	Tyr	Gly	Leu	Pro	Phe	Glu	Lys	Trp	Leu	Leu	Ile	Gly	Ser	Leu	
				380					385					390	
Leu	Phe	Gly	Val	Leu	Phe	Leu	Val	Ile	Gly	Leu	Val	Leu	Leu	Gly	
				395					400					405	
Arg	Ile	Leu	Ser	Glu	Ser	Leu	Arg	Arg	Lys	Arg	Tyr	Ser	Arg	Leu	
				410					415					420	
Asp	Tyr	Leu	Ile	Asn	Gly	Ile	Tyr	Val	Asp	Ile					
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<210> 516
 <211> 2749
 <212> DNA
 <213> Homo Sapien

<220>
 <221> unsure
 <222> 1869, 1887
 <223> unknown base

<400> 516
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ctgaggggacc accggaagta ctgggtgcagg aagggtggga tcctcttctc 200
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cgaaaaacgg ggccccgatg agtctttact gatctctctg ttogtctttc 400
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<210> 517

<211> 332

<212> PRT

<213> Homo Sapien

<400> 517

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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20				25					30	
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35				40					45	
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
				50				55					60	
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Gly	Gln	Glu	Thr	Met	
				65				70					75	

Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	80	85	90
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	95	100	105
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	125	130	135
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	155	160	165
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro	200	205	210
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala	215	220	225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	230	235	240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu	245	250	255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	260	265	270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	275	280	285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	290	295	300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	305	310	315
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val	320	325	330

Ser Ala

<210> 518

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

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<210> 519

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

ctgtcttccc ctgcttggt gtgg 24

<210> 520

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 521

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

ccagtgcaca gcaggcaacg aagc 24

<210> 522

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 522

actaggctgt atgcctgggt gggc 24

<210> 523

<211> 43

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<223> Synthetic oligonucleotide probe

<400> 523

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<210> 524

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe
 <400> 524
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 <210> 525
 <211> 25
 <212> DNA
 <213> Artificial Sequence
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 <400> 528
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<223> Synthetic oligonucleotide probe

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